

GenCore version 5.1.6
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OM protein - nucleic search, using frame_plus.p2n model

Run on: August 19, 2005, 17:54:03 ; Search time 6197 Seconds
(without alignments)
3588.986 Million cell updates/sec

Title: US-09-967-237A-2

Perfect score: 2424

Sequence: 1 MAPICPSPWMLLIPAPAPG.....RRGTGGSVSRPAEVAENGA 459

Scoring table:
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Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 2422767955 residues
Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	2424	100.0	1522	6	AR074439 Sequence
3	2424	100.0	1522	6	AR081119 Sequence
4	2424	100.0	1522	6	AR085316 Sequence

5	2424	100.0	1522	6	AR088064 Sequence
6	2424	100.0	1522	6	AR104223 Sequence
7	2424	100.0	1522	6	AR143487 Sequence
8	2424	100.0	1522	6	AR171392 Sequence
9	2424	100.0	1522	6	AR171563 Sequence
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14	2424	100.0	1552	6	AX333244 Sequence
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42	714	29.5	415	6	AR088079 Sequence
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ALIGNMENTS

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LOCUS Homo sapiens mRNA for renal cell carcinoma associated antigen G250.
DEFINITION AJ010588
ACCESSION AJ010588.1 GI:7327887
VERSION renal cell carcinoma associated antigen G250.
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Carnivora; Homiidae; Homo.
REFERENCE 1 Grabmaier, K., Vlasers, J.L., de Weijert, M.C., Oosterwijk, M.A., van Bokhoven, A., Brakenhoff, R.H., Noessner, E., Mulders, P.A., Merks, G., Fijdor, C.G., Adema, G.J., and Oosterwijk, E. Molecular cloning and immunogenicity of renal cell carcinoma-associated antigen G250
Int. J. Cancer 85 (6), 865-870 (2000)
JOURNAL MEDLINE 20175464
PUBMED 10709109
REFERENCE 2 (bases 1 to 1519)
Oosterwijk, E.
TITLE Direct Submission
AUTHORS Submitted (26-AUG-1998) Oosterwijk E., St. Radboud Academic Hospital Nijmegen, Urological Research Laboratory, Postbus 9101, 6500 HB Nijmegen, THE NETHERLANDS
JOURNAL FEATURES location/Qualifiers
source 1. 1519

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LOCUS AR074439
DEFINITION Sequence 1 from patent US 5955075.
ACCESSION AR074439
VERSION AR074439.1 GI:10001194
KEYWORDS
SOURCE Unknown.
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ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1522)

AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.

TITLE Method of inhibiting tumor growth using antibodies to MN protein

JOURNAL Patent: US 5955075-A 1 21-SEP-1999;

FEATURES Location/Qualifiers

source 1..1522

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LOCUS AR081119

DEFINITION Sequence 1 from patent US 5972353.

ACCESSION AR081119

VERSION AR081119.1 GI:10007847

KEYWORDS

SOURCE

ORGANISM Unknown.

Unclassified.

REFERENCE 1 (bases 1 to 1522)

AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.

TITLE MN proteins, polypeptides, fusion proteins and fusion polypeptides

JOURNAL Patent: US 5972353-A 1 26-OCT-1999;

FEATURES Location/Qualifiers

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ORIGIN

Alignment Scores:

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US-09-967-237a-2 (1-459) x AR081119 (1-1522)

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LOCUS Sequence 1 from patent US 5981711.
DEFINITION AR085316
ACCESSION AR085316
VERSION AR085316.1 GI:10012085
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE MN-specific antibodies and hybridomas
JOURNAL Patent: US 5981711-A 1 09-NOV-1999;
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Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 6
US-09-967-237A-2 (1-459) x AR085316 (1-1522)
Qy 1 MetAlaProLeuGlySerProSerProTyrProLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCTCTGTGTGATCCCGGCCCTCTCCAGGC 72
Qy LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGTGAACTGCTGCTGTCACTGCTCTGTGATGCTGTGCATCCCGAGAGTTG 132
Qy ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATGACGAGGAGATTCCCCCTTGGAGAGGCTCTTCTGGGGAAGATGACCCACTG 192
Qy GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db 193 GGGGAGAGGATTCGCCAGTGAAGAGATTACCCAGAGAGAGATCCACCCGGAGAG 252
Qy GluAspLeuProGlyGlnGluAspLeuProGlyGlyGluAspLeuProGlyValPro 100
Db 253 GAGGATTTACTTGGAGAGAGAGATCTACCTGGAGAGAGATCTACTGAAGTTAACTT 312
Qy LysSerGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGGGGCTCCCTGAAGTTAGAGATCTACTGTTGAGGCTCTCGGA 372
Qy AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140

Db 373 GATCCTCAAGAACCCAGAAATATGSCCAAGAGCAAAAGAGGGATGACCAAGATCAT 432
Qy 141 TTPATGYTGYGlyYAspProProTTProArGVAlSerProAlaCYValAGlyArgPhe 160
Db 433 TGGGGCTATGAGAGGAGACCCGGCCGAGGGGCTGCCAGACCTGGCGGGCGGCTTC 492
Qy 161 GlnSerProValAAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGGTGGATATCCGCCCCCAAGCTCCGGCCCTTCGCGGGCCCTGGCCCCCTG 552
Qy 181 GluLeuLeuGlyPheGlnLeuPheProLeuPheProGlnLeuArgLeuArgAsnAsnGlyHis 200
Db 553 GAACCTCCGGGGCTTCACACTCCCGCGCTCCAGAACTGGCGCTCGCAAGCAATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGlyMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGGAACACTGACCCCTCTCTGGGGCTAGAGAGGCTCTGGGGTCCGGGGGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleTropGlyAlaAlaGlyArgProGlySerGlyHisThr 240
Db 673 CGGGCTCTGACGCTGCACTGTGCACTGGGGGGCTGCAAGTCTCCGGGCTCGAGCACT 732
Qy 241 ValGlnGlyHisArgPheProAlaGlnIleHisValHisIleLeuSerThrAlaPheAla 260
Db 733 GTGGAGGCGCAACCGTTTCCTGCGCGAGATCCAGTGTTCACCTCAGCACCGCCCTTGGC 792
Qy 261 ArgValAAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGGGGCGCGGAGGCGCTGGCGGCTTTCGAG 852
Qy 281 GluGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
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Qy 301 GluGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
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Qy 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProGlyAlaGlnGlyVal 340
Db 973 TTACGCCCTCACTTCCAAATATGAGGGGCTCTGATACACCGCCCTGTGCCAGGGTCTC 1032
Qy 341 IleTTPThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisIleThrLeuSer 360
Db 1033 ATCTGAGACTGTGTTAACCAAGACAGTGAATGCTGAATGCTAAAGCACTCCACCTCTCT 1092
Qy 361 AspThrLeuTropGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCCCTGTGGGAGCTGGTGACTCTGGGCTACAGCTGAACCTTCGAGCGAGCGACT 1152
Qy 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAAspSerSerProArgAla 400
Db 1153 TTGAATGGCGCAGATGATGAGGCTCTCTCCCTGCTGAGTGAAGACAGTCTCGGGCT 1212
Qy 401 AlaGlnProValAlaGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTCCACACTGAATTCCTGCTCGGCTGCTGAGATCTGAAGCCCTGGTATT 1272
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGGCTCTTTTGGCTGTCAACAGCGCTCGGTTCTGTGGCAGATGAGAAAGGAGCAGCA 1332
Qy 441 ArgGlyThrIleGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
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RESULT 5
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DEFINITION Sequence 1 from patent US 5989838.
ACCESSION AR088064
VERSION AR088064.1 GI:10014827
KEYWORDS

SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada, J., Pastorekova, S. and Pastorek, J.
TITLE Immunological methods of detecting MN proteins and MN polypeptides
JOURNAL Patent: US 5989838-A 1 23-NOV-1999;
FEATURES
source location/Qualifiers
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ORIGIN

Alignment Scores:

Pred. No.:	Score:	Length:	Matches:
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Best Local Similarity:	100.00%	Mismatch:	0
Query Match:	100.00%	Indel:	0
DB:	6	Gaps:	0

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Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetCProValHisProGlnArgLeu 40
Db 73 CTCACTGTGCAACGCTGCTGTCACTGCTGTGATGCTGTTCATCCCAAGAGTTGG 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlyIleSerSerGlyGluAspAspProLeu 60
Db 133 CCGGAGTGCAGAGAGATCCCTTGGAGAGGCTTCTGGGAGAGATGACCCACTG 192
Qy 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProGlyGlu 80
Db 193 GCGCAGAGAGATCTGCGCAGAGAGAGATTCACCCAGAGAGAGATCCACCGGAGAG 252
Qy 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyValIlePro 100
Db 253 GAGATCTTACCTGAGAGAGAGATCTCTGAGAGAGAGATCTTACCTGAAGTTAAGCT 312
Qy 101 LysSerGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 120
Db 313 AAATCAGAGAGAGAGGCTCTCTGAAGTGAAGATCTTACTGTTGAGGCTCTGGA 372
Qy 121 AspProGlnGlnProGlnAsnAsnAlaHisArgAspIleGlnGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCGAATATATGCCACAGGAGCAAAAGAGGAGATGACCAAGTCTAT 432
Qy 141 TTPATGYTGYGlyYAspProProTTProArGVAlSerProAlaCYValAGlyArgPhe 160
Db 433 TGGGGCTATGAGAGGCGACCCCGCTGGGGTGTCTCCAGGCTGGCGGGCGGCTTC 492
Qy 161 GlnSerProValAAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGGTGGATATCCGCCCCCAAGCTCCGGCCCTTTCGCGGGCTTCGCGGCCCTG 552
Qy 181 GluLeuLeuGlyPheGlnLeuPheProLeuPheProGlnLeuArgLeuArgAsnAsnGlyHis 200
Db 553 GAACCTCCGGGGCTTCACACTCCCGCGCTCCAGAACTGGCGCTCGCAAGCAATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGlyMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGGAACACTGACCCCTCTCTGGGGCTAGAGAGGCTCTGGGGTCCGGGGGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleTropGlyAlaAlaGlyArgProGlySerGlyHisThr 240
Db 673 CGGGCTCTGACGCTGCACTGTGCACTGGGGGGCTGCAAGTCTCCGGGCTCGAGCACT 732
Qy 241 ValGlnGlyHisArgPheProAlaGlnIleHisValHisIleLeuSerThrAlaPheAla 260

Dh 733 GTGGAAGGCCACCGCTTTCCTCCGAGATCCAGCTGGTTCACTTCAGACCGCCTTTGCC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Dh 793 AGAGTTACAGAGGCTTTGGGGCGCCCGGAGGCTTGCGCTTTGGCGGCTTTCTTGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGluLeuSerArgLeuGluIleAla 300
Dh 853 GAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGAAAGAAATCGCT 912
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Dh 913 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCATCTCGCCTCTGAC 972
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Dh 973 TTCAAGCCGCTACTTCCAAATATGAGGGGTCTTGACTACACCGCCCTTGCCAGGGTGC 1032
Qy 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLysGluLeuHisThrLeuSer 360
Dh 1033 ATCTGACTGTGTTTAAACAGACAGTATGCTGACTGAAGCAGCTCCACACCTCTCT 1092
Qy 361 AspThrLeuTyrProGlyProGlyAspSerArgLeuGluLeuAsnPheArgAlaThrGlnPro 380
Dh 1093 GACACCTGTGGGACCTGTGGACTCTCGCTACAGCTGAACCTTCCAGCGAGCGACGCT 1152
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Dh 1153 TTGGAATGGCGAGAGATTGAGGCTCTTCTCTGCTGAGTGGACACACATGCTTCGGGCT 1212
Qy 401 AlaGluProValGluLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Dh 1213 GCTGAGCGCACTCCAGCTGAATTCCTGCTGTGCTGCTGATCAATCTTACGCCCTGGTTTTT 1272
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGluMetAspArgGlnHisArg 440
Dh 1273 GGCTCTCTTTTGTGTGCACAGCGGTGCGTCTCTTGTGAGATGAAGAAGCGACAGAGA 1332
Qy 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Dh 1333 AGGGGAACCAAGCGGTGTGAGCTTACGCCACAGCAAGTATGCGCAGACTGAGAGCC 1389

RESULT 6
ARI04223 1522 bp DNA linear PAT 14-FEB-2001
LOCUS Definition 1 from patent US 6093548.
ACCESSION ARI04223
VERSION ARI04223.1 GI:12816931
KEYWORDS
SOURCE Unknown.
ORGANISM Unknown.
REFERENCE 1 (bases 1 to 1522)
AUTHORS Zavada,J., Pastorekova,S. and Pastorek,J.
TITLE Detection and quantitation of KM-specific antibodies
JOURNAL Patent: US 6093548-A 1 25-JUL-2000;
FEATURES
source location/Qualifiers
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ORIGIN
Alignment Scores:
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Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
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Dh 73 CTCACTGTGCAACTGCTGCTGTGATCTGCTGCTCTGATGCTGTCTCATCCCAAGAGTTG 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Dh 133 CCCGGATGCAAGAGGATTCCTCCCTTGAGGAGAGGCTCTCTGGGGAAGATGACCCACTG 192
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Dh 193 GCGAGAGGATGTGCCACTGAAGAGATTCACCAAGAGAGAGATTCACCCGGAGAG 252
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGlyGluAspLeuProGlyValLysPro 300
Dh 253 GAGGATTCACCTGAGAGAGAGGATCTACCTGGAGAGAGAGATCTACTGAAGTTAACTC 312
Qy 101 LysSerGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Dh 313 AAATCAGAAAGAGAGGCTCCTGAAGTTAGAGGATCTACTGTTGAGGCTCTCGGA 372
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlyGlyAspAspGlnSerHis 140
Dh 373 GATCTCTAAGAAACCCAGAAATTAATGCCACAGAGGACAAAGAGGAGATGCACAGATCAT 432
Qy 141 TrrArgTyrGlyGlyAspProProTrrProArgValSerProAlaCysAlaGlyArgPhe 160
Dh 433 TGGCGCTATGAGAGCGACCGGCTTGCGCGGAGGTGCCACAGCTGCGGGGCGGCTTC 492
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Dh 493 CAGTCCCGGTGATATCCGCCCCAGCTGCGGCTTCGCCGCGGCGCTGCCCGCTG 552
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnArgHis 200
Dh 553 GAACTCTGGGCTTCAGAGCTCCGCGCGCTCCAGAACTGGCGCTGGCAACAATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Dh 613 AGTGTCAATGACCTCGCTCTCTGGGCTAAGATGGCTTGGGTCCCGGGCGGAGTAC 672
Qy 221 ArgAlaLeuGluLeuHisLeuHisTrrGlyAlaAlaGlyArgProGlySerGluHisThr 240
Dh 673 CGGAGCTGTGAGCTGATGTGCACTGGGGGGCTGCAAGTGTGCCGGCTGGAGCACACT 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Dh 733 GTGGAAGGCCACCGTTTCCTGCGGAGATCCAGTGGGTTCACTCAGACACGCGCTTGGC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Dh 793 AGAGTTACAGAGGCTTTGGGGCGCCCGGAGGCTTGCGCTTTGGCGGCTTTCTTGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGluLeuSerArgLeuGluIleAla 300
Dh 853 GAGGGCCCGGAAGAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGAAAGAAATCGCT 912
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Dh 913 GAGGAAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCATCTCGCCTCTGAC 972
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Dh 973 TTCAAGCCGCTACTTCCAAATATGAGGGGTCTTGACTACACCGCCCTTGCCAGGGTGC 1032
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Dh 1033 ATCTGACTGTGTTTAAACAGACAGTATGCTGACTGAAGCAGCTCCACACCTCTCT 1092
Qy 361 AspThrLeuTyrProGlyProGlyAspSerArgLeuGluLeuAsnPheArgAlaThrGlnPro 380

KEYWORDS	Unknown.
SOURCE	Unknown.
ORGANISM	Unknown.
REFERENCE	Unclassified.
AUTHORS	1 (bases 1 to 1522)
TITLE	Zavada, J., Pastorekova, S. and Pastorek, J.
JOURNAL	MN gene and protein
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Pred. No.:	6 65e-118
Score:	2424.00
Percent Similarity:	100.00%
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Db	73 CTCACCTGTGCACTGCTGCTGTCACTGCTGCTTTCTATGCTGTCCATCCCGAGGTTG 132
OY	41 ProArgMetGlnGluAspSerProLeuGlyGlyIleSerSerGlyIuAspAspProLeu 60
Db	133 CCCCAGATGACAGAGGATTCCCCCTTGGAGGAGGCTCTTCTGGGAAATGACCCACTG 192
OY	61 GlyGluGluAspLeuProSerGlnGluAspSerProArgGluGluAspProProGlyGlu 80
Db	193 GCGGAGGAGATCTGCCAGTAAAGGATCCACCGAGAGGAGATCCACCCGAGAG 252
OY	81 GluAspLeuProGlyGlyIuAspLeuProGlyGlyIuAspLeuProGluValIysPro 100
Db	253 GAGGATCTACCTGGAGGAGGATCTACCTGGAGAGAGATCTACTGTAAGTTAAGCCT 312
OY	101 LysSerGlnGluGlnGlySerLeuIysLeuGluAspLeuProThrValGluAlaProGly 120
Db	313 AAATCAGAAAGAGGGCTCCCTGAAGTAAAGAGATCTACTGTTGAGGCTCTGGA 372
OY	121 AspProGlnGluProGlnAsnAsnAlaHisArgAspIysGluGlyAspAspGlnSerHis 140
Db	373 GATCTCTCAAGAACCCCGAATATATGCCCAAGGACAAAGAGGGATGACCAAGATCAT 432
OY	141 TTPArgTyrGlyIysAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
Db	433 TGGCCCTATGGAGGGGACCCGCCCTGGCCCCGGGTGTCCCAAGCTGCGGGGCCCTTC 492
OY	161 GlnSerProValAspIleArgProGlnLeuAlaIlePheCysProAlaLeuArgProLeu 180
Db	493 CAGTCCCGGTGATATCCGCCCCAGACTGCGGCTTGCCCCGGGCCCTGCCCCCCCTG 552
OY	181 GlnLeuLeuGlyPheGlnLeuProProLeuProGluIleuArgLeuArgAsnGlyHis 200
Db	553 GAACCTCTGGGCTTCAGCTCCGCGGCTCCCAAGACTGGCGCTGGCAATGGGCAC 612
OY	201 SerValGlnLeuThrLeuProProGlyIleuGluMetAlaLeuGlyIleProGlyArgGlyTyr 220
Db	613 AGTGTGCAACTGACCCCTGCTCTCGGTGCTAAGATGCTCTGGTCCCGGGCGGAGTAC 672
OY	221 ArgAlaLeuGlnLeuHisIleuHisIleTPGlyValAlaGlyArgProGlySerGluHisIle 240
Db	673 CCGGCTCTGCACTGATTCGACTGGGGGGGCTGCAAGGTGCTCCGGGCTCGAGACACT 732
OY	241 ValGlnGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260

Db	733	GTGGAAGGCCACGCTTTTCCCTGCGGAGATCCACGTGGTTCACTCCACACCGGCTTTGGC	792
QY	261	ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu	280
Db	793	AGAGTTGACGAGGGCTTTGGGGCGGCCGGAGAGGCTGGCCGGTTGGCCGCTTCTGGAG	852
QY	281	GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluAla	300
Db	853	GAGGGCCCGAAGAAAACAGTGCTTAAGACAGTTCGTCTCCCTTGGAAAGAAATCGCT	912
QY	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	913	GAGAAAGGCTCAGAGACTCAGGTCCCGAGGACTGAGCATATCTGCATCTGGCCCTTCAGAC	972
QY	321	PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProGlyAlaGlnGlyVal	340
Db	973	TTGACCGCTACTCTCCAAATAGAGGGGCTCTGACTACACCGCCCTTGCCAGGGGTCTC	1032
QY	341	IleTyrThrValPheAsnGlnThrValMetLeuSerAlaGlyGlnLeuHisThrLeuSer	360
Db	1033	ATCTGAGACTGTTTAACAGACAGTGAATGCTGAGTCTAAAGCAGCTCCACACCTCTCT	1092
QY	361	AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
Db	1093	GACACCTGTGGGAGCCTGTGACTCTCCGCTTAAGCTGAACCTTCCAGGACGACACCT	1152
QY	381	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla	400
Db	1153	TTGAATGGGCGAGATTTGAGGCTCTCTTCCCTGCTGAGATGACACACATCTCTCGGGCT	1212
QY	401	AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
Db	1213	GCTGAGCGACGTCACGCTGAATTCCTGCTGCTGCTGCTGATGACATCTAGCCCTGGTGT	1272
QY	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgTyrGlnHisArg	440
Db	1273	GGCTCTCTTTTGGTGTGCACCAAGGCTGCGCTCTTCTGTGCAGATGAGAAAGGACACAGA	1332
QY	441	ArgGlyThrIlysglyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459
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DEFINITION	Sequence 1 from patent US 6297051.		PAT 17-DEC-2001
ACCESSION	ARI71563		
VERSION	ARI71563.1	GI:17910513	
KEYWORDS	.		
SOURCE	Unknown.		
ORGANISM	Unknown.		
REFERENCE	Unclassified.		
AUTHORS	1 (bases 1 to 1522)		
TITLE	Zavada,J., Pastorekova,S. and Pastorek,J.		
JOURNAL	MN gene and protein		
FEATURES	Patent: US 6297051-A 1 02-Oct-2001;		
source	Location/Qualifiers		
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Query Match:	6		
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US-09-967-237A-2 (1-459) x ARI71563 (1-1522)			

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Oy	21	LeuThVaG1nLeuLeuLeuSerLeuLeuLeuMetProVa1h1sProG1nAtrLeu	40
Db	73	CTCACTGTGCMACTGCTGCTGTCACTGCTGCTTCTGTATGCTGTCCATCCCCAGAGGTTG	132
Oy	41	ProAtrMeG1nG1uAAsPserProLeuG1yG1ySerSerG1yG1uAAsPProLeu	60
Db	133	CCCCGGATGCAGAGGATTCCTCCCTTGGAGAGGAGCTCTTCTGGGGAAGATGACCACTG	192
Oy	61	G1yG1uG1uAAsPLeuProSerG1uG1uAAsPserProAtrG1uG1uAAsPProProG1yG1u	80
Db	193	GCGGAGAGAGATCTGCCAGTAAAGAGATTCACCAAGAGAGAGAGATTCACCCGGAGAG	252
Oy	81	G1uAAsPLeuProG1yG1uG1uAAsPLeuProG1yG1uG1uAAsPLeuProG1uA1lysPro	100
Db	253	GAGGATCTTACTCGGAGAGAGATCTTACTGAGAGAGAGATCTTACTGTAAGTTAAGCTT	312
Oy	101	LysSerG1uG1uG1uG1ySerLeuLySLeuG1uAAsPLeuProThVaG1uA1aProG1y	120
Db	313	AAATCAGAAAGAGAGGCTCCCTGAAATTAAAGATCTACTCTGTGTAGGCTCTCGGA	372
Oy	121	AsPProG1nG1uProG1nAAsnAAsnA1h1sAtrAsPlyG1uG1yAAsPAsPInsR1s	140
Db	373	GATCTCTCAAGAACCCCGAATATATGCCACAGGGAACAAAGAGGATGACCGAGATCAT	432
Oy	141	TPAATGTATG1yG1yAAsPProProTTPProAtrVa1SerProA1aCyA1aG1yAtrPhe	160
Db	433	TGGCCCTATGAGGGGACCCGCCCTGGCCCCGGGATCTCCACCTTGGCGGGCCGCTTC	492
Oy	161	G1nSerProVa1AsP1eAtrPProG1nLeuA1aA1aPheCyAsPProA1aLeuAtrPProLeu	180
Db	493	CAGTCCCGGGTGGATATCGCCCCAGACTGCGCGCTTGTGCCCGGCCCTCGGCCCTCG	552
Oy	181	G1uLeuLeuG1yPheG1nLeuProProLeuProG1uLeuAtrG1uAtrG1nAAsnG1yH1s	200
Db	553	GAACCTCTGGGGCTTCAGCTCCGCCGCTCCCAAGACTGGCTGGCAACATATGCCAC	612
Oy	201	SerVa1G1nLeuThLeuProProG1yLeuG1uMetA1aLeuG1yProG1yAtrG1yUTr	220
Db	613	AGTGTGCACTACCTGCTCTCTGGGCTTAAAGATGCTCTGGGTCCCGGGCGGAGTAC	672
Oy	221	AtrG1aLeuG1nLeuH1sLeuH1sTrPQ1yA1aA1aG1yAtrProG1ySerG1uH1sThr	240
Db	673	CGGGCTGTCACTGATGTGCACTGGGGGGGCTGCAGGTCGTCTCGGGGCTCGAGCACACT	732
Oy	241	ValG1uG1yH1sAtrPheProA1aG1u1eh1sVal1aH1sLeuSerThralaPheA1a	260
Db	733	GTGGAAAGGCACCGTTTCCCTGCCGAGATCCAGTGTGTCACTCAGCACCGCTTTGGCC	792
Oy	261	AtrGValAAsPQ1a1aLeuG1yAtrPProG1yG1yLeuA1aValLeuA1aA1aPheLeuG1u	280
Db	793	AGAGTTGACGAGAGCCCTGGGGGCGCCGGAGAGGCTGGCGGTGTGGCCCGCTTTCGAG	852
Oy	281	G1uG1yProG1uG1uAAsnSerA1aTrG1uG1nLeuLeuSerAtrG1uG1u1eA1a	300
Db	853	GAGGGCCCCGAGAAABAACAGCTGCTTATGAGCACTTCTGCTTGGTGAAGAAATCGCT	912
Oy	301	G1uG1uG1ySerG1uThG1nValProG1yLeuAAsP1eSerA1aLeuLeuProSerAAsP	320
Db	913	GAGGAAGGCTCAGAACTCAGAGTCCAGAGACTGGACATATCTGTCACTCCGCTCTGAC	972
Oy	321	PheSerAtrG1yPheG1nTrG1uG1ySerLeuThThProProCyA1aG1nG1yVal	340
Db	973	TTCACCCGCTACTCTCCAAATATAGAGGGGTCTGTGACTACACCGCCCTGTGCCAGGGGTGC	1033
Oy	341	11eTPThValPheAAsnG1nThVa1MetLeuSerA1yLeuG1nLeuH1sTrThLeuSer	360
Db	1033	ATCTGGAAGCTTTTAAACAGACAGTGA1GCTGAAGTCTTAAAGAGGCTTCACACCTCTCT	1093
Oy	361	AsPThrLeuTrPQ1yProG1yAAsPserAtrG1uG1nLeuAAsnA1aThrG1nPro	380

Dd	1093	GACACCCTGTGGGAACTCGTGTACTCTTCGGCTTAQAGCTGAATCTCCAGCAGCCAGCCT	1152
Oy	361	LeuhangiYarqValIleGlualSerPheProAlaGIYValAapSerSerProArgAla	400
Dd	1153	TTGATATGGGCAAGTAGATTGAAGGCCTCCTTCCTCCTGAGATGACAGACGATCCTCGAGCT	1212
Oy	401	AlaGIUProValIGlnLeuAenSerCysLeuAlaAlaGIYAspIleLeuAlaLeuValPhe	420
Dd	1213	GCTAGGCCAGTCGACGTGAATTTCTGTGCTGTGCTGTGTGACATCTTAAGCCCTGTTTTT	1272
Oy	421	GIyleuLeuPheAlaValAlThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Dd	1273	GGCCTCCTTTTGTGCTGTCAACCAAGCTCGCCTTCTTGTGCAGATGAGAAGCACACACGA	1332
Oy	441	ArgGIYThrlysgGIYValISerTYrArgProAlaGIUValAlaGIUthrGIYAla	459
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RESULT 10			
Locus	BD243152	1522 bp	DNA linear PAT 17-JUL-2003
DEFINITION	MN gene and protein.		
ACCESSION	BD243152		
VERSION	BD243152.1 GI:33052922		
KEYWORDS	JP 2002528085-A/1.		
SOURCE	Homo sapiens (human)		
ORGANISM	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
REFERENCE	Zavada,J., Pastorekova,S. and Pastorek,J. 1 (bases 1 to 1522)		
AUTHORS	Javada,J., Pastorekova,S. and Pastorek,J.		
TITLE	MN gene and protein		
JOURNAL	Patent: JP 2002528085-A 1 03-SEP-2002;		
COMMENT	INSTITUTE OF VIROLOGY OS Homo sapiens (human) PN JP 2002528085-A/1 PD 03-SEP-2002 PF 23-OCT-1999 JP 2000578465 PR 23-OCT-1998 US 09/177776, 23-OCT-1998 US 09/178115 PT JAN ZAVADA, SILVIA PASTOREKOVA, JAKOMIR PASTOREK PC C12N15/09,A61K38/00,A61K39/395,A61K39/395,A61K48/00,A61P35/00, PC C07K14/47, PC C1201/02,G01N33/566// (C12Q1/02,C12R1.91),C12N15/00,A61K37/02		
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Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
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Dd	13	ATGgctcccccctgtgtccccagccctcgctcctcttggtagatcccgccctcgctccagac	72
Oy	21	LeuthralyGlnleuleuleusefLeuleuleuleumefProValHIsproGlnargLeu	40
Dd	73	CTCAtcgtgcAcactgcctcctcActcctcgtcttttgAnngcctgttcATccccAGAGGtTG	132

41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
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Qy 61 G1GluGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProGlyGlu 80
Db 193 GGCAGAGAGATCTGCCAGTGAAGAGATTACCCAGAGAGAGATCCACCCGAGAG 252
Qy 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlyGluAspLeuProGlyValIlePro 100
Db 253 GAGGATCTACCTGAGAGAGAGATCTACCTGAGAGAGATCTACCTGAAGTTAACTCCT 312
Qy 101 LysSerGlnGluGlnGlySerLeuLysLeuGluAspLeuProThrValIleGluAlaProGly 120
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Db 433 TGGGCGCATGGAGCGACCCGCCCTGGCCCGGGTGTCCCGAGCTCGGGGGCGCGCTTC 492
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Qy 221 ArgAlaLeuGlnLeuHisIleuHisIleProGlyValAlaIleGlyArgProGlySerGlnHisThr 240
Db 673 CGGGCTGTGAGCTGCACTGCACTGGGGGCTGCAAGTGTGCTGCTGGAGAAATGCT 732
Qy 241 ValGlnGlyHisArgPheProAlaGlnIleHisValValHisIleuSerThrAlaPheAla 260
Db 733 GTGAGAGGCAACGCTTCCCTGCGGAGATCCAGTGTTCACCTCAGACACGCTTGGC 792
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Db 793 AGAGTTGACAGGCTTGGGGCGCCGAGAGGCTGGCCGCTTGGCGCTTCTGAG 852
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Db 853 GAGGCGCCGAGAAACAGTGCCTATGACAGATTTGCTGCTGCTGGAGAAATGCT 912
Qy 301 GlnGlnGlySerGlnThrGlnValIleProGlyLysAspIleSerAlaLeuLeuProSerAsp 320
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Qy 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
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Qy 341 IleTrpThrValPheAspGlnThrValMetLeuSerAlaLysGlnLeuHisIleThrLeuSer 360
Db 1033 ATCTGAGCTGTGTTAACTCAGACAGTATCTGATCTGATGACAGCTCCACCCCTCTCT 1092
Qy 361 AspThrLeuTrpGlyProGlyLysSerArgLeuGlnLeuAspPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGCTCGGTGACTCTCGGCTACAGCTGAATTCGAGAGAGAGGAGCT 1152
Qy 381 LeuAspGlyArgValIleGlnAlaSerPheProAlaGlyValLysSerSerProArgAla 400
Db 1153 TTGAATGGGAGAGATTGAGGCTCTCTCCCTGCTGAGTGAAGAGATGCTCGGGCT 1212
Qy 401 AlagluProValGlnLeuAspSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420

Db 1213 GCTGAGCGACTCCAGCTGATTCCTGCTGGCTGGTACATCTTACCGCTGTTT 1272
Qy 421 G1LysLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTTTTGTCTGTCAACAGCTCGCTTCTTGTGTGAGATGAGAGAGGACACAGA 1332
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LOCUS CQ834035
DEFINITION Sequence 71 from Patent EP1439393.
ACCESSION CQ834035
VERSION CQ834035.1 GI:50833640
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1 Aistle, J.H., Boardman, L.A., Bugart, L.J., Burgess, C.C., Catino, T.J.,
AUTHORS Dwyer, P., Huntress, M., Johnson, K.A., Lewis, M.E., Maimonis, P.J.,
Myerow, S.H., Brown-Shimer, S.L., Thiagalingam, A., Thibodeau, S.N. and
Molino, G.A.
TITLE Detection methods using TIMP 1 for colon cancer diagnosis
JOURNAL Patent: EP 1439393-A 71 21-JUL-2004;
Bayer Healthcare LLC (US); MAYO FOUNDATION FOR MEDICAL EDUCATION
AND RESEARCH (US)
FEATURES
source Location/Qualifiers
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/organism="Homo sapiens"
/mol_type="unassigned DNA"
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ORIGIN
Alignment Scores:
Pred. No.: 6,78e-118 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
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Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnAArgLeu 40
Db 103 CTACCTGTGCACTGCTGCTGTCACTGCTGCTTCTATGCTGTCCATCCCGAGAGTTG 162
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 163 CCCCGATGAGAGAGATTCCCTTGGGAGAGGCTCTTCTGGGAAATGACCCACTG 222
Qy 61 G1GlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db 223 GGGGAGAGAGATGTGCCAGTGAAGAGATTCAACCCAGAGAGAGATCCACCCGAGAG 282
Qy 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProThrValIleGluAlaProGly 100
Db 283 GAGGATCTACTGTAAGAGAGATCTACTGAGAGAGAGATCTACTGAAGTTAAGCT 342
Qy 101 LysSerGlnGlnGlySerLeuLysLeuGluAspLeuProThrValIleGluAlaProGly 120
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Qy 121 AspProGlnGluProGlnAspAspAlaHisArgAspLysGlnGluAspAspGlnSerHis 140

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KEYWORDS	Homo sapiens (human)
SOURCE	Homo sapiens
ORGANISM	Eumetazoa; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE	1
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,
TITLE	Horrigan, S., Soppet, D. R. and Weaver, Z.
JOURNAL	Cancer gene determination and therapeutic screening using signature gene sets
FEATURES	Patent: WO 0194629-A 516 13-DEC-2001;
source	Avalon Pharmaceuticals (US)
Location/Qualifiers	1. .1552
ORIGIN	/organism="Homo sapiens" /mol_type="unassigned DNA" /db_xref="taxon:9606"

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Pred. No.:	6.78e-118
Score:	2424.00
Percent Similarity:	100.00%
Best Local Similarity:	100.00%
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DB:	6
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Db	103	CTCACTGTGGAAACTGCTGCTGTCACTGCTGTTCTGATGGCTGTTCATCCCAAGGTTG	162
QY	41	ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGlyLeuAspProLeu	60
Db	163	CCCCGGATGCAAGAGGAGATTCCCCCTTGGAGAGAGGCTCTTCTGGGGAAGATGACCCACTG	222
QY	61	GlyGlnGluAspLeuAspSerGlnGluAspSerProArgGlnGluAspProProGlyGly	80
Db	223	GGCAGAGAGAGATCTGCCCAATGAAAGAGATTCAACCAGAGAGAGATCCACCCGAGAG	282
QY	81	GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGluValLysPro	100
Db	283	GAGATATTACTGTGAGAGAGAGATCTACCTGGAAGAGAGATCTCACTGAAGTTAAACCT	342
QY	101	LysSerGlnGlnGlnGlySerLeuLysLeuGlnLysAspLeuProThrValGlnAlaProGly	120
Db	343	AAATTCAGAGAGAGAGGCTCCCTGAATTGAGAGATTCACTACTGTGTGAGGCTCCGGA	402
QY	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlyGlyAspAspGlnSerHis	140
Db	403	GATCCTCAAGAACCCCAAGATTAAAGCCACAGGAGCAAAAGAGGAGATGACCAAGATCAT	462
QY	141	TrpArgTyrGlyGlyAspProProTTrpProArgValSerProAlaCysAlaGlyArgPhe	160
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QY	161	GlnSerProValAspLLeArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu	180
Db	523	CAGTCCCGGATGATATCCGCCCACTGCGCCCTTCTGGCCCCGGGCTGGCCCCCTG	582
QY	181	GluLeuLeuGlnPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis	200
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QY	221	ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlnHisThr	240
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Db	763	GTGGAGGCGCACCGTTTCCCTGCGGAGATCCACGGTTCACCTCGACACCGCTTGGCC	822
QY	261	ArgValAlaArgGlnAlaLeuGlnYArgProGlyGlyLeuAlaValAlaAlaPheLeuGln	280
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QY	281	GlnGlyProGlnGlnGlnAsnSerAlaTrpGlnGlnLeuLeuSerArgLeuGlnGlnIleAla	300
Db	883	GAGGGCCCGGAGAAAGAAACAGTCCATAGCAGATTGGCTGCTCGCTTGGAAAGAAATCGCT	942
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Db	943	GAGGAGGCTCAGAGACTCAGGTTCCCGAGAGACTGACATATCTGCACCTCCTCCCTGCAC	1002
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Db	1003	TTCAGCCGCTACTTCCATATAGAGGGGCTCTGACTACACCGCCCTGGCCAGGGTGTCTC	1062
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Db	1063	ATCTGACATGTTGTTTAAACAGACAGTGAATGCTGAGTGTAAAGCAGCTCCACACCTCTCT	1122
QY	361	AspThrLeuThrProGlyProGlyAspSerArgLeuGlnLeuAsnPheAlaAlaThrGlnPro	380
Db	1123	GACACCCCTGTGGGGGACCTGTGACTCTCGGCTTACAGCTGAACCTCCGAGCAGACAGCTT	1182
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Db	1183	TTGATAGGCGCAGATGATTGAGGCTCTCTCTCTGCTGAGAGTGACAGAGTCTCTCGGGCT	1242
QY	401	AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
Db	1243	GCTGAGCCAGTCCAGCTGAATTCTCGCTGCTGGCTGTGACATCTTAGCCCTGTGGTTTTT	1302
QY	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1303	GGCTCCCTTTTGGCTGTCACACAGCTCGCGTTCCTGTGCAGATGAGAGAGGACACACAGA	1362
QY	441	ArgGlyThrIleGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla	459
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ACCESSION	AX332607		
VERSION	AX332607.1		GI:18123241
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ORGANISM			
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	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
REFERENCE			
AUTHORS	1 Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G.,		
	Horrigan, S., Soppet, D.R. and Weaver, Z.		
TITLE	Cancer gene determination and therapeutic screening using signature		
JOURNAL	gene sets		
	Patent: WO 0194629-A 3116 13-DEC-2001;		
	Avalon Pharmaceuticals (US)		
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ORIGIN			

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Percent Similarity:	100.00%	Conservative:	0
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DB	103	CTCACTGTGCAACTGCTGCTGTCACTGTGCTTGTGATGCTGTGTCATCCCGAAGGTTG	162
QY	41	ProArgMetG1nuaSpSerProLeuG1yG1ySerSerG1yG1uAspAspProleu	60
DB	163	CCCCGGATGCGAGGAGATTCCCTTGGGAGAGAGCTCTTCTGGGGAAGATGACCCACTG	222
QY	61	G1yG1nG1uAspLeuProSerG1nG1uAspSerProArgG1uG1uAspProG1yG1u	80
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DB	283	GAGATCTACTGGAGAGAGAGATCTTACTTGAGAGAGAGATCTCACTGAAGTTAACTT	342
QY	101	LysSerG1nG1nG1nG1ySerLeuLeuLeuG1uAspLeuProThrVal1G1uVal1aProG1y	120
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DB	463	TGGCGCTATGAGAGCGACCCGCCCTGGGCCGGGGTGTCCCAAGCTCGCGGGCGGCTTC	522
QY	161	G1nSerProVal1aAsp1eArgProG1nLeuVal1a1aPheCybPro1a1aLeuArgProleu	180
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DB	643	AGTGTGCACTGACCCCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCCGGGCGGGAATAC	702
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QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerProArgAla 400
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Db 1243 GCTGAGCAGTCCAGTCACTGAATTCCTGCTGGCTGTGGAGACATCTTGGCTTTT 1302
QY 421 GlyLeuLeuPheAlaValIleThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCCTCTTTTGTGCTGTACACGCGCTCGCTTCTTGTGCAATGAGAAGGACGACAGA 1362
QY 441 ArgGlyThrIlyArgGlyValIleSerTyrArgProAlaGluValAlaGluThrGlyVala 459
Db 1363 AGGGAGACCAAGGGGGTGTGAGTACCGCCAGAGAGTACCGCAAGCTGGAGCC 1419
RESULT 14
AX333244 1552 bp DNA linear PAT 09-JAN-2002
LOCUS Sequence 3753 from Patent WO0194629.
DEFINITION AX333244
ACCESSION AX333244
VERSION AX333244.1 GI:18123878
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominiidae; Homo.
REFERENCE 1
AUTHORS Young, P.E., Augustus, M., Carter, K.C., Edner, R., Endress, G.,
Horrikan, S., Soppet, D.R. and Weaver, Z.
TITLE Cancer gene determination and therapeutic screening using signature
JOURNAL gene seq
Patent: WO 0194629-A 3753 13-DEC-2001;
Avalon Pharmaceuticals (US)
FEATURES
source 1..1552
location/Qualifiers
1..1552
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
ORIGIN
Alignment Scores:
Pred. No.: 6,78e-118 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
US-09-967-237a-2 (1-459) x AX333244 (1-1552)
QY 1 MetaLapProLeuCyPProSerProTTPLeuProLeuLeuIleProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGTGCCAGCCCTGTGCTCTCTGTGATCCCGGCCCTGTCTCAAGC 102
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACGTGGCAACGCTCTGTCTGTCTTGTGATGCTGTCTCATCCCGAGGGTTG 162
QY 41 ProArgMetGlnGluAspSerProLeuGlnGlyIleSerSerGlyGluAspAspProLeu 60

Db 163 CCCCGAGTCAGAGAGGATTCCTCCCTTGGGAGAGGCTTTCTGGGAGAGATGACCACCTG 222
QY 61 GlyIleGluAspLeuProSerGlyGlnIleAspSerProArgGlyGlnIleAspProGlyGlu 80
Db 223 GCGCGAGAGAGATCTGCCAGATGAAGAGATTCAACCAAGAGAGAGATCCAACCCGAGAG 282
QY 81 GluAspLeuProGlyGlyIleGluAspLeuProGlyGlyIleGluAspLeuProGlyValIleAspPro 100
Db 283 GAGGATCTACCTGGAGAGAGAGATCTTACCTGAGAGAGATCTTACCTGAAATTAGCTT 342
QY 101 LysSerGlyGlnGlyGlySerLeuIleLeuGlnAspLeuProThrValIleAlaProGly 120
Db 343 AAATAGAGAGAGAGGCTCTCCCTGAGATTAGAGATCTACTGTTAGAGGCTCTGGA 402
QY 121 AspProGlnIleProGlnAsnAsnAlaHisArgAspIlyGlyIleAspArgIleSerHis 140
Db 403 GATCTCTCAAGAAACCCCAAAATATGCCCAAGAGGACAAAGAGAGGATGACCAAGATCAT 462
QY 141 TTPArgTyrGlyIleAspProProTTPProArgValIleSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGGCTATGGAGGAGCCGCTGTGCGCGGGGTGTCCAGGCTGTGCGGGCCGCTTC 522
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCGCGGATATCCGCGCCAGCTCGCGCTTCTGCGCGGCTCGCGGCTCGCGGCTG 582
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlyLeuAlaGlyLeuArgAsnAsnGlyHis 200
Db 583 GAACTCTGGGCTTCCAGCTCCCGCTCCAGAACTGCGCTCGCGCAACAATGGCCAC 642
QY 201 SerValGlnLeuThrLeuProProGlyIleLeuIleAlaGlyProGlyArgGlyIleThr 220
Db 643 AGTGTCAACTGACCTGCTCTGTGGGTACAGATGCTGTGGGTCCGGGGGAGATAC 702
QY 221 ArgAlaLeuGlnLeuHisLeuHisIleTPGlyAlaAlaGlyArgProGlySerGlyHisThr 240
Db 703 CGGGCTGTGAGCTGCATCTGCATCTGCAGGCGGCTGAGGCTGTCGGGCTCGGAGACACT 762
QY 241 ValGlyIleHisArgPheProAlaGlyIleHisValAlaHisLeuSerThrAlaPheAla 260
Db 763 GTGGAGGCGCACCGTTTCTCGCGAGATCCACGTTGTTCCTCAGCAGACCGCTTTC 822
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyIleLeuAlaValIleLeuAlaAlaPheLeuGln 280
Db 823 AGAGTGAAGAGGCTTGTGGGCGCCCGGAGGCTGTGGCGGTGTGGAG 882
QY 281 GluGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlyIleAla 300
Db 883 GAGGCGCGGAGAAAGAACAGTCTATGACAGATTGCTGCTCGTTGGAGAAATGCT 942
QY 301 GluGlyIleSerGlyIleThrGlnValIleProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAGGCTCAGAGACTCAGGTCTCCAGGACTGACATATCTGACTCTCCCTCTAC 1002
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAGCCCGCTACTCTCAATATGAGGAGTCTTGACTACACCGCTGTGGCCAGGAGTGC 1062
QY 341 ILeTPThrValPheAsnGlnThrValMetLeuSerAlaGlnLeuHisThrLeuSer 360
Db 1063 ATCTGGACTGCTTTAAACAGACACTGATGCTGATGCTTAAGCACTCCACACCTCTCT 1122
QY 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCCGTGGGGAGCTGTGTACTTCGGCTACAGCTGAACCTTCGAGCGACGAGCT 1182
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1183 TTGAATGGGCGAGATTTGAGGCTCTTCCTGCTGAGATGACAGCACTCTGGGCT 1242
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420

Db	1243	GGTAGCGCAAGTCCAGCTGAATTCCTGCTGCTGCTGTGTGTCACATCCCTAGCCCTGTTT	1302
Oy	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetAlaArgGlnHisArg	440
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Oy	441	ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459
Db	1363	AGGGGACCAAGGGGGGTGTAGCTACCGCCACAGCAGGTAGCCGAGACTGGAGCC	1419
RESULT 15			
AX336174			
LOCUS	AX336174	1552 bp	DNA
DEFINITION	Sequence 6683 from Patent WO0194629.		linear
ACCESSION	AX336174		
VERSION	AX336174.1		
KEYWORDS	GI:18126893		
SOURCE			
ORGANISM	Homo sapiens (human)		
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
AUTHORS	Young, P.E., Augustus, M., Carter, K.C., Ebner, R., Endress, G., Horriگان, S., Soppet, D.R. and Weaver, Z.		
TITLE	Cancer gene determination and therapeutic screening using signature gene sets		
JOURNAL	Patent: WO 0194629-A 6683 13-DEC-2001;		
FEATURES	Avalon Pharmaceuticals (US)		
SOURCE	Location/Qualifiers		
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	/mol_type="unassigned DNA"		
	/db_xref="taxon:9606"		
ORIGIN			
Alignment Scores:			
Pred. No.:	6,78e-118	Length:	1552
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0
US-09-967-237A-2 (1-459) x AX336174 (1-1552)			
Oy	1	MetAlaProLeuCysProSerProTyrLeuProLeuLeuProAlaProGly	20
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Oy	21	LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu	40
Db	103	CTCACTGTGCAACTGTCTGTCTCACTGTGCTTGTGATGCTTGCATCCCAAGGTTG	162
Oy	41	ProArgMetGlnGluAspSerProLeuGlyGlyLeuSerGlyGluAspAspProLeu	60
Db	163	CCCCGGATGCGAGGAGATTTCCCTTGGGAGAGAGCTCTTCTGGGAAAGATGACCCACTG	222
Oy	61	GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu	80
Db	223	GGCGAGGAGGATCTGCCAGTGAAGAGGATTCACCCAGAGGAGGATCCACCCGGAGAG	282
Oy	81	GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGluValLysPro	100
Db	283	GAGATCTACTGAGAGGAGATCTACTGAGAGGAGATCTACTGAAATTAAAGCT	342
Oy	101	LysSerGlnGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly	120
Db	343	AAATCAGAAAGAGGGCTCCCTGAAGTGAAGATCTACTGTTGGAGCTCTGGA	402
Oy	121	AspProGlnGluProGlnAspAsnAlaHisArgAspLysGlnGluAspAspGlnSerHis	140
Db	403	GATCTCTAAGAACCCCAAGATTAATGATCCACAGGAGCAAGAGGGAGATGACCAAGATCAT	462

[illegible]

Search completed: August 20, 2005, 00:09:25
Job time : 6227 secs

XX	RESULT 1	
XX	ADL70155	
XX	ID	ADL70155 standard; cDNA; 1380 BP.
XX	AC	
XX	ADL70155;	
XX	20-MAY-2004	(first entry)
XX	Human carbonic anhydrase isozyme CA IX coding sequence.	
XX	Human; carbonic anhydrase; tumour; antigen; cytosolic; gene; ss	
XX	Homo sapiens.	
XX		
XX	Key	Location/Qualifiers
XX	FT	1..1380
XX	CDS	/*tag= b
XX	FT	/product= "Carbonic anhydrase CA IX"
XX	FT	1..110
XX	sig_peptide	/*tag= a
XX	FT	111..1377
XX	mat_peptide	/*tag= c
XX	FT	
XX	PN	
XX	MO2004017923-A2.	
XX	PD	
XX	04-MAR-2004.	
XX	25-AUG-2003; 2003WO-US026612.	
XX		

PR 23-AUG-2002; 2002US-040577P.
 PR 22-AUG-2003; 2003US-00646934.
 XX
 PA (CHIR) CHIRON CORP.
 XX
 PI Wong J, Winter J, Lalehzadeh G, Warne R;
 XX
 DR WPI; 2004-226730/21.
 DR P-PSDB; ADL70156.
 XX
 PT Identifying an agent capable of inhibiting carbonic anhydrase (CA)
 PT activity of CA IX polypeptide for treating cancers, comprises combining a
 PT test agent with a cell expressing CA IX and assessing CA inhibitory
 PT activity of the test agent.
 XX

PS Example 6; SEQ ID NO 1; 82pp; English.

XX The present sequence is the coding sequence for human carbonic anhydrase
 CC 180zyme IX (CA IX), an N-glycosylated membrane-associated glycoprotein
 CC also known as the MN or G250 tumour-associated antigen. The invention
 CC relates to compositions and methods useful in inhibiting CA IX-
 CC preneoplastic or neoplastic cells. The inhibitors are especially
 CC antagonistic anti-CA IX antibodies and other inhibitory agents that
 CC target the carbonic anhydrase activity of CA IX on these cells. The
 CC antibodies, or their antigen-binding fragments, are specifically reactive
 CC with an inhibitory epitope of CA IX. Screening assays for identifying
 CC such inhibitory agents are provided. The antibodies, their antigen-
 CC binding fragments, and other inhibitory agents are useful in the
 CC treatment of cancers characterized by the expression of CA IX, such as:
 CC head and neck cancers; gynaecological cancers including ovarian,
 CC cervical, vaginal, endometrial and vulval cancers as well as
 CC gynaecological precancerous conditions such as metaplastic cervical
 CC tissues and condylomas; gastrointestinal cancers such as stomach, colon
 CC and oesophageal cancers; urinary tract cancer such as bladder and kidney
 CC cancers; skin cancer; liver cancer; prostate cancer; lung cancer; and
 CC breast cancer.
 XX

SQ Sequence 1380 BP; 257 A; 428 C; 420 G; 275 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1 47e-130	Length:	1380
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	12	Gaps:	0

US-09-967-237a-2 (1-459) x ADL70155 (1-1380)

QY 1 MetAlaBProLeuCySPSePrProTPrLeuProLeuLeuIleProAlaProAlaProGly 20
 Db 1 ATGGCTCCCTGTCGCCAGCCCTGGCTCCCTCTGTGATCCCGGCCCTGCTCCAGGC 60
 QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnHisArgLeu 40
 Db 61 CTCACTGTGAACCTGCTGTCACTCTCTCTGTGATGCTTCATCCCAAGAGGTTG 120
 QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyIleSerSerGlyGluAspAspProLeu 60
 Db 121 CCCCAGATGAGAGGATTTCCCTTGGAGAGAGCTCTTCTGGGAGAGATGACCCACTG 180
 QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
 Db 181 GCGGAGAGGATGCGCCAGTGAAGAGATTCAACCCAGAGAGGAGATTCACCCGAGAG 240
 QY 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyGlnValIlePro 100
 Db 241 GAGGATCTACTCTGAGAGAGGAGATCTACCTGAGAGAGAGATCTAACCTGAAGTTAACT 300
 QY 101 LysSerGlnGluGlnGlySerLeuIleLeuGlnAspLeuProThrValGlnAlaProGly 120
 Db 301 AATTCAGAAAGAGGGCTCCCTGAGATTAGAGGATCTACTCTTGAGGCTCTCGGA 360

QY 121 AspProGlnGluProGlnIleuAsnAlaHisArgAspLysGlnGlyAspArgGlnSerHis 140
 Db 361 GATCTCTCAAGAACCCCAAGATTAATGCCACAGAGGACAAAGAGGAGTACCAAGATCAT 420
 QY 141 TrpArgTyrGlyGlyAspProProTPrProArgValSerProAlaCysAlaGlyValArgPhe 160
 Db 421 TGGCGCTATGAGAGCCACCCGCTGGCCCGGGGTGTCCCACTGCGGGCCGCTTC 480
 QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuAspProLeu 180
 Db 481 CAGTCCCGGTGATATCCGCCCCCAAGCTGCGGCTCTTCCGCCGCGCCCTCCCTG 540
 QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnArgHis 200
 Db 541 GAACTCCTGGGCTTCCAGCTCCCGGCTCCAGAACTGGCGCTGCGCAACATGGCCAC 600
 QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyValArgGlyTyr 220
 Db 601 AGTGTCAACTGACCCCTGCTCTGGGCTAGAGATGGCTCTGGGTCCCGGCGGAGTAC 660
 QY 221 ArgAlaLeuGlnLeuHisIleHisTyrGlyAlaAlaGlyArgProGlySerGlnHisThr 240
 Db 661 CGGGCTCTGCACTGCATCTGCACCTGGGGGCTGCAAGTCTGCGGGCTGAGACACT 720
 QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisValValHisLeuSerThrAlaPheAla 260
 Db 721 GTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGTTCACCTCAGCACCCGCTTGGCC 780
 QY 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln 280
 Db 781 AGAGTTCAGAGGCTTGGGGCCCGGGAGGCTGACCTGTTGGCCGCTTTCGAG 840
 QY 281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
 Db 841 GAGGGCCCGGAAGAAACAGTGCCTATGAGCACTTCTGCTGTGGAGAAATCGCT 960
 QY 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
 Db 901 GAGGAAGGCTCAAGAGCTCAGTCCAGGACTCGACATATCTGACTCTCCCTCTGAC 960
 QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
 Db 961 TTCAAGCCGACTACTCAATATGAGGGGTCTCTGACTACACGCGCTGTGCCAGGGTTC 1020
 QY 341 IleTyrThrValPheAsnGlnThrValIleLeuSerAlaIleGlnLeuHisThrLeuSer 360
 Db 1021 ATCTGAGCTGTGTTTAACCAAGACAGTATGCTGAGTCTAAGCAGCTCCACACCTCTCT 1080
 QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
 Db 1081 GACACCTGTGGGGGACCTGTGACTCTCGGCTACACTGAACCTTCGAGGAGAGAGCCT 1140
 QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
 Db 1141 TTGAATGGCGGATGATTTGAGGCTCTCTCTCTGAGTGAAGCACTCTCCGGCT 1200
 QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
 Db 1201 GCTGAGCAGATCCAGCTGAATTCCTGCTGGCTGCTGCTGCTGCTGCTGCTGCTGCT 1260
 QY 421 GlyLeuLeuPheAlaValThrSerValAlaAlaPheLeuValGlnMetArgArgGlnHisArg 440
 Db 1261 GGCCTCTTTTCTGTCTGACCAAGCTGCGTTTCTTGTGTGAGTGAAGAGGCGACAGA 1320
 QY 441 ArgGlyThrIleArgGlyValIleSerTyrArgProAlaGlnValAlaGlnThrArgAla 459
 Db 1321 AGGGAACCAAGAGGGGTGTGACTACCGCCACGACAGAGTACCCAGACTGAGGCC 1377

RESULT 2
 ADP54000
 ID ADP54000 standard; DNA; 1392 BP.
 XX
 AC ADP54000;

XX 26-AUG-2004 (first entry)
XX Human carbonic anhydrase IX coding sequence.
XX da; gene; cytosolic; cancerous disease; carbonic anhydrase IX protein;
XX gene therapy; anticancer; tumor imaging; scintigraphy;
XX neoplastic disease; carcinoma; head and neck cancer; mesodermal tumor;
XX neuroblastoma; retinoblastoma; osteosarcoma; Ewing's sarcoma; melanoma;
XX metabolism.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 13..1392
XX /tag= a
XX /product= "carbonic anhydrase IX"
XX MO2004048544-A2.
XX 10-JUN-2004.
XX 26-NOV-2003; 2003WO-US037783.
XX 26-NOV-2002; 2002US-0429089P.
XX 22-JUN-2003; 2003US-0489473P.
XX 28-OCT-2003; 2003US-0515104P.
XX (FARB) BAYER HEALTHCARE.
XX (VIRO-) INST VIROLOGY.
XX (SUPU-) SUPURAN C.
XX (SCOZ/) SCOZZAFAVA A.
XX Supuran C, Scozzafava A, Pastorekova S, Pastorek J;
XX WPI: 2004-460762/43.
XX P-PSDB; ADP53999.
XX Treating mammal for pre-cancerous or cancerous disease such as head and
XX neck cancer, involves administering composition comprising compound such
XX as inhibitors of MN/carbonic anhydrase IX enzymatic activity to mammal.
XX
XX Disclosure: SEQ ID NO 2; 106pp; English.
XX
XX The invention relates to a method of treating (M1) a mammal for a pre-
XX cancerous or cancerous disease, where the disease is characterized by
XX overexpression of MN/carbonic anhydrase (CA) IX protein, by administering
XX a composition comprising a compound (CC) to the mammal, where CC is
XX chosen from organic and inorganic molecules, and CC is determined to be a
XX potent inhibitor of MN/CA IX enzymatic activity in a screening assay.
XX (M1) is useful for treating a mammal such as human for a pre-cancerous or
XX cancerous disease. The CA IX inhibitor of (M1) is useful for: (1)
XX diagnostic or prognostic method, including imaging methods, and for gene
XX therapy; (11) in the development of drugs possessing anticancer
XX properties; (111) for imaging tumors by scintigraphy, and useful for
XX treating wide variety of pre-neoplastic/neoplastic diseases including
XX carcinomas, such as mammary, colorectal, urinary tract, ovarian, uterine,
XX cervical, endometrial, squamous cell and adenocarcinomas, head
XX and neck cancers, mesodermal tumors such as neuroblastomas and
XX retinoblastomas, sarcomas such as osteosarcomas and Ewing's sarcoma and
XX melanomas; (11) basic and pre-clinical research, for studying the
XX regulation of CA IX enzyme activity, for studying the role of CA IX in
XX tumor growth and metabolism, and for studying the role of CA IX in
XX response to treatment by drugs, radiation and inhibitors. This sequence
XX corresponds to the coding sequence for the human carbonic anhydrase IX
XX enzyme of the invention.
XX
XX Sequence 1392 BP; 260 A; 433 C; 423 G; 276 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.48e-130 Length: 1392
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0
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QY 1 MetalProLeuCySPSeSerProTLeuProLeuLeuLeuProAlaProAlaProGly 20
DB 13 ATGGCTCCCTGTGCCCCAGCCCTGCTCCCTCTGTGATCCCGCCCTGCTCAAGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
DB 73 CTCACGTGCAACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGlyAspAspProLeu 60
DB 133 CCGCGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 192
QY 61 GlyGluGluAspLeuProSerGlyGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 252
QY 81 GluAspLeuProGlyGlyGluAspLeuProGlyGlyGluAspLeuProGlyValIysPro 100
DB 253 GAGGATCTAAGCTGGAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 312
QY 101 LysSerGlyGluGlyGlySerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
DB 313 AAATCAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
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DB 433 TGGCGCTATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
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QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlyLeuArgLeuArgAsnAlaHis 200
DB 553 GAACTCTGGGCTTCAGCTCCCGCGCTCCCAAGACTCCGCTCGGAGCAATGGCCAG 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
DB 613 AGTGCAACTGACCTGCTCTGAGGCTAGAGATGGCTTGGGTCGCGGCGGAGATAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisIleTrpGlyAlaAlaGlyArgProGlySerGlnHisThr 240
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QY 241 ValGlnGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
DB 733 GTGAAAGCCACCGTTTCCCTGCGGAAGTCAAGCTGTCACTCAAGACCGCCCTTCC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValAlaAlaAlaPheLeuGlu 280
DB 793 AGAGTTGACGAGGCTTGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGluAla 300
DB 853 GAGGAGCCGGAAGAAAGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
DB 913 GAGGAAGGCTAGAGACTCAAGTCCCAAGACTGGAACATATGCACTCTCCCTCTAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrProProCysValGlnGlyVal 340
DB 973 TTCAGCCGCTACTTCATATGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAGGAG 1032

Oy	341	TETPTTTRVAlPHeAnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer	360
Db	1033	ATCTGGACTGTGCTTTAACCAACAGACTGATGCTGAGCTTAAGACAGCTCCACACCTCTCT	1092
Oy	361	AsPTHTLeuTRPGlyProGlyAspSerArgLeuGlnLeuAnpheArgAlaThrGlnPro	380
Db	1093	GACACCCCTGTGGGGAGCTGTGACTCTCGGTACAGCTGAACCTCCGAGCGACAGCT	1152
Oy	381	LeuAnGlyAArgValIleGlnAlaSerPheProAlaGlyValAlaPseSerProArgAla	400
Db	1153	TTGATATGGGCAGATGATTGAGGCGCTCTCCCTGCTGTGAAGTGACAGAGATCTCGGCGCT	1212
Oy	401	AlaGlnPProValGlnLeuAnSerCysLeuAlaIaGlyAspIleLeuValaLeuValPhe	420
Db	1213	GCTGAGCCAGATCCAGCTGAATTCCTGCTGCTGCTGTGATCATCTTACCTGGTTT	1272
Oy	421	GlyLeuLeuPheAlaValaThrSerValaAlaPheLeuValaGlnMetArgArgGlnHisArg	440
Db	1273	GGCTCTCTTTTGTGCTGTACACAGCGTCGCTTCTTGTCAGATGAGAAAGGACACAGCA	1332
Oy	441	ArgGlyThrIysGlyGlyValaSerTyrArgProAlaGluValaIaGluThrGlyAla	459
Db	1333	AGGGAAACCAAGGGGGGTGAGCTACCGCCACAGAGAGATGAGGAGACTGTGAGCC	1389
RESULT 3			
AD573098	ID	AD573098 standard; cDNA, 1519 BP.	
AC	AD573098;		
XX	18-NOV-2004	(first entry)	
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XX			
DE		Human kidney tumour specific cDNA, SEQ ID 1695.	
XX			
KW		Human; ss; kidney tumour; kidney cancer; cytostatic; gene therapy;	
RW		T-cell; immune response.	
XX			
OS		Homo sapiens.	
XX			
PN		US2003109434-A1.	
PD		12-JUN-2003.	
XX			
PF		19-MAR-2002; 2002US-00102524.	
XX			
PR		19-MAR-2001; 2001US-0277245P.	
XX		21-DEC-2001; 2001US-0343340P.	
XX			
PA		(CORI-) CORIXA CORP.	
PI		Algate PA, Mannion J, Gaiger A, Gordon B, Harlocker SL;	
XX		WPI; 2002-759855/82.	
DR			
XX			
PT		New isolated polynucleotides and polypeptides, useful for detecting the	
PT		presence of, and treating cancer, particularly kidney cancer by	
PT		stimulating T-cells specific for a tumor protein, and stimulating immune	
PT		response in a patient.	
XX			
PS		Claim 1; SEQ ID NO 1695; 78pp; English.	
XX			
CC	The invention relates to a new isolated polynucleotide (a Human kidney		
CC	tumour specific cDNA) comprising any one of the 1855 sequences identified		
CC	in the specification (or their complements, degenerate variants,		
CC	sequences consisting of at least 20 contiguous residues them, sequences		
CC	that hybridize to them under highly stringent conditions or sequences		
CC	having at least 75 or 90% sequence identity to the 1855 sequences. Also		
CC	included are detecting/determining the presence of cancer in a patient,		
CC	stimulating an immune response in a patient; treating kidney cancer in a		
CC	patient, an isolated polypeptide encoded by one of the 1855 sequences, an		
CC	expression vector comprising the polynucleotide operably linked to an		
CC	expression control sequence, a host cell transformed/transfected with the		

CC	vector) can isolated antibody (or its antigen-binding fragment) that
CC	specifically binds to the protein, a fusion protein comprising at least
CC	one the proteins, stimulating and/or expanding T-cells specific for a
CC	tumour protein, an isolated T-cell population comprising the T-cells, a
CC	composition comprising a first component (such as a carrier or
CC	immunostimulant) and a second component (comprising one of the
CC	polynucleotides), the polypeptides, an antibody, T-cell or an antigen-
CC	presenting cell that expresses the polynucleotide) and a diagnostic kit
CC	comprising at least one of the oligonucleotides, or at least one antibody
CC	and a detection reagent comprising a reporter group. The polynucleotides,
CC	polypeptides, antibodies and antigen-presenting cells are useful for
CC	detecting the presence of, and treating cancer, particularly kidney
CC	cancer by stimulating and/or expanding T-cells specific for a tumour
CC	protein, and stimulating immune response in a patient. The present
CC	sequence is one of the Human kidney tumour specific cDNAs. Note: The
CC	sequence data for this patent did not form part of the printed
CC	specification, but was obtained in electronic format directly from USPTO
CC	at seqdata.uspto.gov/sequence.html?DocID=20030109434.
XX	
SQ	Sequence 1519 BP; 296 A; 456 C; 453 G; 314 T; 0 U; 0 Other;
Alignment Scores:	
Pred. No.:	1,62e-130 Length: 1519
Score:	2424.00 Matches: 429
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0
DB:	Gaps: 7 0
US-09-967-237A-2 (1-459) x ADS73098 (1-1519)	
OY	1 MetalapProleuCysProSerProTrieuProLeuLeuIleProAlaProAlaProGly 20
Db	10 ATGGCTCCCCGTGTGCCCAAGCCCCTCGCTCCTCTTGATGATCCGGCCCCCTGTCACAGGC 69
OY	21 LeuthrVaIGlnLeuLeuLeuSerLeuLeuLeuMeuProValHisProGlnArgLeu 40
Db	70 CTCATGTGCAACTGTCTGTCTGTCACTGCTGCTTGTGATCCGTCCATCCCAAGAGTTG 129
OY	41 ProArqMetcGInLaSpSerProLeuGlyGlyGlySerSerGlyGluLaSpApProleu 60
Db	130 CCCGGATGCAAGAGATTCCCCCTTGGGAGAGAGCTTTCTGGGGAAGATGACCACATG 189
OY	61 GlytGluGlaSpleuProSerGluGluLaSpSerProArgGluGluLaSpProProGlyGlu 80
Db	190 GGCGAGGAGGATCTGCCCAAGTAAGAATTCACCACAGAGAGAGATCCACCCGAGAG 249
OY	81 GluaSpleuProGlyGluGluLaSpLeuProGlyGluGluLaSpLeuProGluValLysPro 100
Db	250 GAGCATCTAACTCGAGAGAGAGATCTTACTCGAGAGAGATCTTACTGAAGTTAAGCT 309
OY	101 LysSerGluGluGlyGlySerLeuLysLeuGluLaSpleuProThrValGluAlaProGly 120
Db	310 AAATCAGAGAAAGAGGGCTCCTCGTAGTTAGAGATCTTAACCTACTGTTAGGCTCCTGGA 369
OY	121 AspProGInGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGInserHis 140
Db	370 GATCTCCAAGAACCCCAAGATATATCCCAAGAGACAAAGAGGGATACAAGATCAT 429
OY	141 TPATgTyrgLygLYASPProPOTriPeProARgVALISerProALCYsaLAglArgphe 160
Db	430 TGGCGCTATGGAGGCAACCGCCCTGGCCCGGGGTGTCCCCAGCTGCGCGGGCGCTTC 489
OY	161 GlnSerProValAspLIearGProGlnLeuAlaAlaPheCysProAlaAleuarGProleu 180
Db	490 CAGTCCCGGAGGAAATCCGCCCAAGCTCGCGGCTTCTGCGCGACTTGCGCCCCCTG 549
OY	181 GluLeuLeugLyPheGlnLeuProProleuProGluLeuArgLeuArgAsnaGlyHis 200
Db	550 GAATCCTCGGGCTTCACACTCCCGCGCTCCAGAACTGCGCTCGCAACAATGGCCAC 609
OY	201 SerValGlnLeuThreuProProGlyLeuGluMetAlaLeuGlyVProGlyArgGlyIyr 220

Db 610 AGTGTCAACTGACCTGCTCTCTGAGATGAGTCTGAGTCCCGGAGGAGTAC 669
Qy 221 ATGATALEUAGLNUHIALEUHIATTPGLVALAALAGLYAARGPROGLYSEGLUHSIHR 240
Db 670 CGGGCTCTGACAGCTGATCTGACATGGGGGGCTGAGAGTCTGCCGGCTCCGAGCACACT 729
Qy 241 VALGUGLYHIAARGPHEPROLAAGLUTLEHISVALAHISLEUSERTHRALPHEA 260
Db 730 GTGAGAGCCACCGTTTCCCTGCCAGATCCAGTGGTTCACTCAGACCCGCTTTGCC 789
Qy 261 ARGVALAARGVALALEUGLYAARGPROGLYSEGLUVALAVALLEUVALAAPHLEUGLU 280
Db 790 AGAGTTGACGAGGCTTGGGGGGCCGGGAGGCTGGCCGCTGGTGGCCCTTTCTGGAG 849
Qy 281 GLUGLYPROGLYUANSERVALATYRGUINLEULEUSERVALARGLEUGLUHLEA 300
Db 850 GAGGAGCCCGGAGAAACAGTGCCTATGACAGTGTGCTGTCTGGTGAAGAAATTCCT 909
Qy 301 GLUGLYSERGLUTHRGLINVALPROGLYUANSERVALALEULEUPROSERASP 320
Db 910 GAGGAGGCTCAGAGACTCAGGCTCCAGACTGACATHTCTGACTCTGCTCCCTCTGAC 969
Qy 321 PHESEARGTYRPHGLNTRYRGUPLYSELEUTHRTTHRPROCYAALAGLNGLYA 340
Db 970 TTCAAGCCGCTACTTCCATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGGGTGT 1029
Qy 341 ILETPTHTVALPHEAENGINTHRVALMETLEUSERVALYVGLINLEUHISTRLEUSER 360
Db 1030 ATCTGAGACTGTGTTTAAACAGACAGTGAATGCTGAATGCTTAAGCACCTCCACCTCTCT 1089
Qy 361 ASPHTLEUTHRPGLYPROGLYASPSERARGLEUGLNUANSERPHARGALATHRGANPRO 380
Db 1090 GACACCCCTGTGGGACCTGGTGACTCTGGCTACGCTGAACCTCCGAGCAGCAGGCT 1149
Qy 381 LEUANGLYARGVALILEGLUALASERPHROAGLYVALASPSERSETPROARGLA 400
Db 1150 TTGAATGGGCGAGTATGAGGCTCTTCCCTGTGAGTGAACAGACAGTCTCTGGGCT 1209
Qy 401 ALAGUPTROVALGINTLEANSERVALAAGLYAAPPILLEUVALAVALPHE 420
Db 1210 GCTAGGCAAGTCCAGCTAAATTCCTGCTGCTGTGACATCTCTAGCCCTGATTTT 1269
Qy 421 GLYLEULEUPHEAALAVATHSERVALALAPHELEUVALGIMETARGARGLNHISARG 440
Db 1270 GGCTCTCTTTTTCCTGACACAGGCTCCGCTTCTCTTGACAGTAGAAGCAGACACGA 1329
Qy 441 ARGGLYTHRYSGLYVALSERTYRARGPROLAGUVALAAGLUTHRGLYLA 459
Db 1330 AGGGGAACCAAGGGGCTGTAGGTAACGCCAGAGAGTACCGAGACTGGAGCC 1386
RESULT 4
AAT09186
ID AAT09186 standard; cDNA, 1522 BP.
AC AAT09186;
XX
AC AAT09186;
XX
DT 25-MAR-2003 (revised)
DT 19-AUG-1996 (first entry)
XX
DE MUTU putative oncogene MN cDNA.
XX
XX MUTU; endogenous; cellular component; MN; Hela cell; diagnosis;
KM lymphocytic choriomeningitis virus; LCMV; putative oncogene; treatment;
KM neoplastic; pre-neoplastic; disease; anticense therapy; antibody;
KM vaccine; vertebrate; immunisation; ss.
XX
OS Homo sapiens.
XX
FH Key Location/Qualifiers
FT CDS 13..1392
XX /*tag= a
XX ,MO9534650-A2.

XX 21-DEC-1995.
PD 15-JUN-1995; 95WO-US007628.
XX 15-JUN-1994; 94US-00260190.
XX 07-JUN-1995; 95US-00477504.
PR 07-JUN-1995; 95US-00481658.
PR 07-JUN-1995; 95US-00485049.
PR 07-JUN-1995; 95US-00485862.
PR 07-JUN-1995; 95US-00485863.
PR 07-JUN-1995; 95US-00486756.
PR 07-JUN-1995; 95US-00487077.
XX
PA (CIBA) CIBA CORNING DIAGNOSTICS CORP.
PA (VIRO-) INST VIROLOGY.
XX Zavada J, Pastorekova S, Pastorek J;
XX MPI, 1996-043679/05.
DR P-PSDB; AAR88058.
XX
XX MN gene, protein and nucleic acid fragments - used as primers and probes
PT in the detection of MN antigens and antibodies, and in the treatment of
PT (pre)neoplastic disease.
XX
XX Claim 1; Fig 1; 102pp; English.
XX
XX The present sequence is the full length MUTU endogenous cellular
CC component, MN, cDNA clone, which was isolated from lymphocytic
CC choriomeningitis virus (LCMV) infected Hela cells. Persistent LCMV, the
CC exogenous MUTU transmissible agent (MX), infection increases the
CC expression level of the MN gene. MN is a putative oncogene, and can
CC therefore be used in the development of prods. for the diagnosis and
CC treatment of neoplastic (NP), or pre-NP diseases. NP diseases can be
CC treated using DNA antisense to MN transcribed mRNA, anti-MN protein
CC antibodies can be used for the diagnosis NP or pre-NP diseases and a
CC vaccine contg. immunogenic amounts of the MN protein can be used to
CC immunise a vertebrate against a NP disease associated with MN antigen
CC expression. (Updated on 25-MAR-2003 to correct PR field.)
XX
XX Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;
XX
XX Alignment Scores:
Pred. No.: 1.62e-130 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 2 Gaps: 0
US-09-967-237A-2 (1-459) x AAT09186 (1-1522)
Qy 1 Meta1APROLEUCYSPROSERPROTRPLEUPROLEULEU1LEPROALA1PROALA1PROGLY 20
Db 13 ATGGCTCCCTGTCGTCACAGCCCTGGCTCCTCTGTGATGCCGGCCCTGCTCCAGGC 72
Qy 21 LEUTHRYVALGINTLEULEUSERLEULEULEULEUWETPROVALHISPROGLNARGLEU 40
Db 73 CTCACGTGCAACCTGCTGCTCTCACTGCTGCTTGTGATGCCCTGTCCATCCCAAGGTTG 132
Qy 41 PROARGMETGNGLUASPSERPROLEUGLYGLYGLYSESERGLYGLYUASPSERPROLEU 60
Db 133 CCCCAGATGACGAGAGATTCCTCCCTTGGAGAGAGGCTCTTGGGAGAGATGACCCACTG 192
Qy 61 GLYGLYUASPSERPROSERGLYUASPSERPROARGGLYUASPSERPROGLYGLY 80
Db 193 GCGGAGGAGATCTGCCAGATGAAGAGATTACCCAGAGAGAGATTCCACCCGAGAG 252
Qy 81 GLUASPLEUPROGLYGLYUASPSERPROGLYGLYUASPLEUPROGLYVALYVPRO 100
Db 253 GAGGATCTACCTGAGAGAGAGATCTTACCTGAGAGAGAGATTCTTCAAGTTAAGCTT 312

[illegible]

AA16540	
ID	AAA16540 standard; cDNA; 1522 BP.
XX	
AC	AAA16540;
XX	
DT	16-JUN-2000 (first entry)
XX	
DE	Human MN protein encoding cDNA SEQ ID NO:1.
XX	
KW	Human; MN protein; MN gene; oncogene; carbonic anhydrase; tumour;
KW	oncogenesis; diagnosis; neoplastic disease; cancer; carcinoma;
KW	MN/CA IX isoenzyme; ds.
XX	
OS	Homo sapiens.
PX	
PN	US6027887-A.
XX	
PD	22-FEB-2000.
XX	
PF	24-JAN-1997; 97US-00787739.
XX	
PR	21-OCT-1992; 92US-00964589.
PR	30-DEC-1993; 93US-00177093.
PR	15-JUN-1994; 94US-00260190.
PR	07-JUN-1995; 95US-00477504.
PR	07-JUN-1995; 95US-00481658.
PR	07-JUN-1995; 95US-00485049.
PR	07-JUN-1995; 95US-00485862.
PR	07-JUN-1995; 95US-00485863.
PR	07-JUN-1995; 95US-00486756.
PR	07-JUN-1995; 95US-00487077.
XX	
PA	(SLSC-) SLOVAK ACAD SCI INST VIROLOGY.
XX	
PI	Pastorek J, Zavada J, Pastorekova S;
XX	
PT	WPL; 2000-194827/17.
DR	P-PsDB; AAY53228.
XX	
PT	Nucleic acid based assay for diagnosing a wide variety of
PT	pneumoplastic/neoplastic disease comprises screening for the presence of
PT	abnormal MN gene expression in a vertebrate.
XX	
PS	Claim 1; Fig 1; 87pp; English.
XX	
CC	The present invention describes a method of screening for
CC	pneumoplastic/neoplastic disease. The method comprises: (1) determining
CC	whether abnormal MN gene expression is present in a vertebrate; and (2)
CC	if abnormal MN gene expression is determined to be present in the
CC	vertebrate, determining that the vertebrate has a significant risk of
CC	having pneumoplastic/neoplastic disease. The MN gene is an oncogene and
CC	encodes an MN protein (also referred to as MN/CA IX isoenzyme). The MN
CC	protein is a tumour associated carbonic anhydrase isoenzyme. The method
CC	is used for detecting a wide variety of pneumoplastic/neoplastic diseases
CC	in a vertebrate, preferably a human. The disease detected is mammary,
CC	bladder, renal, urinary tract, ovarian, uterine, cervical, endometrial,
CC	vaginal, vulval, prostate, liver, lung, skin, thyroid, pancreatic,
CC	testicular, brain, head and neck, mesodermal, gallbladder, rectal,
CC	duodenal, jejunal, ileal, gastric, pancreatic duct, liver duct, gastric
CC	mucosa, gallbladder epithelium, small intestinal mucosa, colorectal
CC	mucosa, pancreatic duct epithelium or liver duct epithelium
CC	pneumoplastic/neoplastic disease. AAA16540 to AAA16617 and AAY53228 to
CC	AAY53245 represent sequences used in the exemplification of the present
CC	invention
XX	
SO	Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other:
Alignment Scores:	
Pred. No.:	1.62e-130 Length: 1522
Score:	2424.00 Matches: 459
Percent Similarity:	100.00% Conservative: 0
Best Local Similarity:	100.00% Mismatches: 0
Query Match:	100.00% Indels: 0

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DB: 3 Gaps: 0
US-09-967-237a-2 (1-459) x AA16540 (1-1522)
QY 1 MetalaproteinCyseProSeProTrpleuProleuLeuileProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTCTGTGATCCCGGCCCTCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerleuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACTGTGCAACCTGCTCTGTCACTGCTTCTGATGCTCTGATCCCTCCAGAGTTG 132
QY 41 ProArgMetGlnGluAspSerProleuGlyGlySerSerGlyGluAspAspProleu 60
Db 133 CCCCAGATGCAAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGAGAGATACCCACTG 192
QY 61 GlyGluGluAspLeuProSeSerGlyGluAspSerProArgGluGluAspProGlyGlu 80
Db 193 GCGGAGAGATCTGCCAGTGAAGAGATTCACCAGAGAGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGlyGluGluAspLeuProGlyGlyGluAspLeuProGlyValLysPro 100
Db 253 GAGATCTCACTCGAGAGAGATCTACCTGAGAGAGATCTACCTGAAGTTAAGCT 312
QY 101 LysSerGluGluGluGlySerleuLysleuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACTACTGTGAGGCTCTTGA 372
QY 121 AspProGluGluProGluAsnAsnAlaHisArgAspLysGlyGluAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCAAGATATATGCCACAGAGCAAAAGAGGATGACCAAGTCA 432
QY 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGGGCTATGAGAGGAGCCCGCTGGCCCGGGGTGTCCCAAGCTTGGCGGGCGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaIlePheCysProAlaLeuArgProleu 180
Db 493 CAGTCCCGGCTGGATATCCGCCCCAGCTCCGCCCTTCTGCCCCGCCCCCTGGCC 552
QY 181 GluLeuLeuGlyPheGlnLeuProProleuProGluLeuArgLeuArgAsnGlnHis 200
Db 553 GAATCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTCGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyPheGlyArgGlnTyr 220
Db 613 AGTGTGCAACTGACCTCTCTCTGGGCTAGAGATGCTCTGGGCTCCGGGGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisIleuHisIleTrpGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CCGGCTCTGACGCTGATCTGCACTGGAGGCTGCAAGTCTCGAGCTCGAGCACA 732
QY 241 ValGluGlyHisArgPheProAlaGlnIleHisValHisIleLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGAGATCCAGTGTTCACCTCAGACCGCCCTTGG 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGGGCGCCGGAGGCTGGCGGTGGTGGCGCCCTTCTGGAG 852
QY 281 GlyGlyProGluGluAsnSerAlaTrpGluGlnLeuLeuSerArgLeuGlnIleAla 300
Db 853 GAGGCCCCGAGAAACAGTGCCTATAGCACTTGTCTCTCGCTTGGAGAAATCCCT 912
QY 301 GlyGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGCTCCAGAGACTGACATATCTGCACTCTGCGCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerleuThrTrpProProCysAlaGlnIleVal 340
Db 973 TTTCAGCCCTCTCTCAATATGAGGGGTCTCTGATTAACCGCCCTGTGGCCAGGCTTC 1032
QY 341 IleTrpThrValPheAsnGlnThrValIleLeuSerAlaValGlnLeuHisThrLeuSer 360

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Db 1033 ATCTGAGACTGTGTTTAACTCAGACAGTATGCTGAGTGTCTTAAGCACTCCACCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCCCTGTGGGGACCTGTGACTCTCGGCTACAGCTGAACCTCCGAGCAGCAGCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCCAGATGATTAAGGCTCTCTTCCCTGCTGAGTGGACAGCACTCTCGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCAGACTCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTCTTTTGGCTGTGACCAAGGCTCCGCTTCTGTGCAAGATGAGAAAGCAGCAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrTrpProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAGACCAAGGGGGTGTGAGCTACCGCCAGCAGAGTACCGAGACTGAGGCC 1389

RESULT 6
AA52459
ID AA52459 standard; cDNA; 1522 BP.
AC AA52459;
DE 25-SEP-2000 (first entry)
XX Human MN cDNA.
XX MN protein; tumour associated cell adhesion molecule; oncoprotein;
XX proteoglycan domain; PG domain; carbonic anhydrase; CA domain;
XX abnormal expression; neoplastic disease; cancer; gene therapy; ss.
XX Homo sapiens.
XX Key Location/Qualifiers
XX CDS 13..1392
XX FT /*tag= a
XX FT /product= "Human MN protein"
XX
XX MO200024913-A2.
XX
XX 04-MAY-2000.
XX
XX 22-OCT-1999; 99MO-US024879.
XX
XX 23-OCT-1998; 98US-00177776.
XX
XX 23-OCT-1998; 98US-00178115.
XX
XX (FARB ) BAYER CORP.
XX PA (VIRO-) INST VIROLOGY.
XX
XX Zavada J, Pastorekova S, Pastorek J;
XX WPI; 2000-350752/30.
XX
XX P-PSDB; AAB03005.
XX
XX A molecule which specifically binds to a site on MN protein (oncoprotein)
XX PT and prevents adhesion of vertebrate cells to the protein, useful for
XX PT treating preneoplastic or neoplastic diseases such as cancer.
XX
XX Example 1; Fig 1A-C; 154p; English.
XX
XX The invention relates to the inhibition of cell adhesion mediated by the
XX MN oncoprotein (also known as the MN/CA IX isoenzyme or the MN/G250
XX protein). The MN protein is a tumour-associated adhesion molecule which
XX comprises a proteoglycan-like (PG) domain (AAB03017) which contains the
XX protein's binding site, and a carbonic anhydrase (CA) domain (AAB03018).
XX Abnormal expression of the MN protein is associated with tumorigenicity.

```

CC The invention encompasses molecules (e.g., proteins and peptides) which
CC which specifically bind to a site on the MN protein, thereby preventing
CC adhesion of vertebrate cells to the protein in a cell adhesion assay. It
CC also encompasses MN proteins or MN protein fragments which can be added
CC to the extracellular environment to prevent the adhesion of vertebrate
CC cells to each other. The invention also relates to the identification of
CC the binding site of the MN protein and to a method of identifying a site
CC on an MN protein to which cells adhere, comprising testing a series of
CC overlapping peptides from the protein in a cell adhesion assay. The
CC invention encompasses a vector comprising an expression control sequence
CC operatively linked to a nucleic acid encoding the variable domains of a
CC MN-specific antibody, where the domains are separated by a flexible
CC linker peptide (AAS03035) and the vector inhibits the growth of a
CC vertebrate preneoplastic or neoplastic cell that abnormally expresses MN
CC protein. The invention also encompasses a vector comprising a nucleic
CC acid encoding a cytotoxic protein or peptide operatively linked to the MN
CC gene promoter, which inhibits the growth of a vertebrate preneoplastic or
CC neoplastic cell. Also claimed is a repressor complex that binds to the MN
CC gene promoter (AAS2473). MN proteins and peptides, MN-binding proteins
CC and peptides, and expression vectors encoding such proteins and peptides
CC are useful for treating patients with preneoplastic or neoplastic disease
CC (e.g., cancers) associated with or characterised by abnormal MN
CC expression. The present sequence represents cDNA encoding the human MN
CC protein

XX
SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1 62e-130	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	3	Gaps:	0

US-09-967-237A-2 (1-459) x AAS2459 (1-1522)

QY 1 MetAlaProLeuCySPSeSPSeProTTPLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCTCTGTGTGATCCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACTGTGCACTGCTGTGTCACTGCTCTTGTGATGCTTGTCCATCCCGAGAGGTTG 132
QY 41 ProArgMetGlnLeuAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATGAGAGGATTTCCCTTGGAGAGGCTCTTCTGGGAGAGTGAACCCACTG 132
QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db 193 GCGAGAGGAGATCTGCCCACTGAAGAGATTCAACCCAGAGAGAGATCCACCGGAGAG 252
QY 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyValLeuPro 100
Db 253 GAGGATCTTACTCTGAGAGGAGATCTAACCCTGAGAGAGATCTAACCCTGAAGTTAAACCT 312
QY 101 LySerGlnGlnGlnGlnGlnSerLeuLeuGlnAspLeuProThrValGlnAlaProGly 120
Db 313 AAATCAGAAAGAGGCTCCCTGAAGTTAGAGATTTACTTACTGTGAGGCTCCCTGGA 372
QY 121 AspProGlnGlnProGlnAsnAsnAlaHisArgAspLeuGlnGlnAspAspGlnSerHis 140
Db 373 GATCTCTCAAGAACCCGAGATTAATGCCCACAGGGAACAAGGAGGTGACCAAGATCAT 432
QY 141 ThrArgTyrGlnGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGAGAGCGACCGCCCTGGCCCTCCGGGTGTCTCCACCTGGCGGCGCCGTTT 492
QY 161 GlnSerProValAspLeuArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCCCAGCTGCGCCCTTCTGCCCCGCGCTGCGCCCCCTG 552

QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgAsnAsnGlyHis 200
Db 553 GAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGGCTGGGCAACAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGGTGCACTGACCTGCTCTCTGGGCTAGAGATGGCTTGGGTCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisIleTyrGlyAlaAlaGlyArgProGlySerGlyHisIleThr 240
Db 673 CGGGCTCTGAGCTGATCTGCACTGGGGGCTGCAAGTGTGTCGGGCTGGAGCACACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnLeuHisValValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTCACTCCAGCACCGGCTTGGC 792
QY 261 ArgValAspGlnAlaLeuGlnArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGGCCCGGAGGCTGGCCGTGTGGCCGCTTTCTGGAG 852
QY 281 GlyGlyProGlnGlnAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnLeuAla 300
Db 853 GAGGCGCCGAGAAAGAAACAGTGCCTATGAGCACTTGTCTGCTTGGAGAAATCGCT 912
QY 301 GlyGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGTCCAGAGCTGGAATCTGACCTCCCTGCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCAGCGCTACTTCCAAATGAGGGGTCTCTGACTACACGGCCGTGTGCCAGGGTGTG 1032
QY 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaLeuGlnLeuHisIleThrLeuSer 360
Db 1033 ATCTGAGCTGTGTTTAACAGACAGATGATCTAGTGTCAAGCAGCTCCACCTCTCT 1092
QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGACTGTGTGACTCTCGGCTACACTGAATCTCCAGAGGAGCGACCT 1152
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGAGATGATTTGAGGCTCTCTTCCCTGCTGAGTGAACAGACACTCTCGGGCT 1212
QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCAGTCCAGCTGAATTCCTGCTGGCTGCTGCTGATCTTAAGCCCTGTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTCTTTTCTCTGTCAACACGCTGCGCTTCTTGTGCAGATGAGAGGCAACAGA 1332
QY 441 ArgGlyThrIleGlnGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
Db 1333 AGGGAACCAAGAGGGGTGTGAGCTACCGCCCAAGAGGTACCCAGACTGAGACC 1389

RESULT 7
ADG31413
ID ADG31413 standard; cDNA, 1522 BP.
XX
AC ADG31413;
XX
DT 26-FEB-2004 (first entry)
XX
DE Human MN cDNA, SegID 1.
XX
KW human; gene; ss; monoclonal antibody; MN/CA IX; MN; oncogene;
KW carbonic anhydrase 9; CA9; MN/CA9; carbonic anhydrase IX; CA IX; MN/G250;
KW neoplastic tumour; cyostatic; cancer; tumour therapy;
KW anti-tumour vaccine.
XX
OS Homo sapiens.
XX

EN WO2003100029-A2.
 XX
 PD 04-DEC-2003.
 XX
 XX
 PE 22-FEB-2003; 2003WO-US005136.
 XX
 PR 23-MAY-2002; 2002US-0383068P.
 PR 05-DEC-2002; 2002US-0431499P.
 XX
 PA (PARB) BAYER CORP.
 PA (VIRO-) INST VIROLOGY.
 XX
 PI Pastorek J, Pastorekova S, Zatovicova M, Zavada J, Ortova Gut M;
 XX
 DR WPI, 2004-035136/03.
 DR P-PSDB; ADG31414.
 XX
 PT New monoclonal antibody generated from MN/CA IX-deficient mice, where the
 PT antibody binds specifically to human tumor-associated cell adhesion
 PT protein MN/CA IX or polypeptide, useful for diagnosing, prognosing or
 XX treating cancer.
 XX
 XX Disclosure; SEQ ID NO 1; 156pp; English.

ADK41803
ID ADK41803 standard; DNA, 1522 BP.
XX
XX AC ADK41803;
XX
XX DT 06-MAY-2004 (first entry)
XX
XX DE Human MN gene sequence SegID1.
XX
XX KW carbonic anhydrase IX; CA IX; precancerous cell; MN; cancerous cell;
XX human; vertebrate; cytostatic; vaccine; gene therapy;
XX KW renal cell carcinoma; breast cancer; colorectal cancer; de; gene.
XX
XX OS Homo sapiens.
XX
XX FH Key Location/Qualifiers
XX FT CDS 13..1392
XX FT /*tag= a
XX FT /product= "Human MN protein"
XX
XX PN WO2004005348-A1.
XX
XX PD 15-JAN-2004.
XX
XX PF 22-FEB-2003; 2003WO-US005137.
XX
XX PR 23-MAY-2002; 2002US-0383068P.
XX PR 05-DEC-2002; 2002US-0431499P.
XX
XX PA (FARB) BAYER CORP.
XX PA (VIRO-) INST VIROLOGY.
XX
XX PL Zavada J, Pastorekova S, Pastorek J, Zavadova Z;
XX
XX DR WPI; 2004-083500/08.
XX DR P-PSDB; ADK41804.
XX
XX PT New soluble form of the carbonic anhydrase IX (CA IX) protein for
XX screening; diagnosing or prognosing diseases associated with abnormal
XX expression of CA IX protein, e.g. renal cell carcinoma, breast cancer or
XX colorectal cancer.
XX
XX PS Disclosure; SEQ ID NO 1; 159pp; English.
XX
XX CC This invention relates to a novel soluble form of the carbonic anhydrase
XX IX (CA IX) (or MN) protein or CA IX polypeptide which is released from
XX precancerous and/or cancerous cells of a vertebrate into a body fluid.
XX CC The invention may be useful for the development of compounds with a
XX cytosolic activity or a vaccine whilst the disclosed sequences may be
XX used for gene therapy. The protein and method are useful for screening,
XX diagnosing or prognosing diseases associated with abnormal expression of
XX carbonic anhydrase IX protein, such as precancerous and cancerous
XX diseases like renal cell carcinoma, breast cancer or colorectal cancer.
XX CC The monoclonal antibody may also be used for treating or preventing
XX precancerous and cancerous diseases. The present sequence is part of the
XX gene which encodes the human MN protein of the invention.
XX
XX SQ Sequence 1522 BP; 297 A; 458 C; 453 G; 314 T; 0 U; 0 Other;

Alignment Scores:
Pred. NO.:
Score: 1.62e-130 Length: 1522
Percent Similarity: 2424.00 Matches: 459
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 12 Gaps: 0

US-09-967-237A-2 (1-459) x ADK41803 (1-1522)

1 MetAlaProLeuGlyCysPProSerPProTyrPLeuProLeuLeuIleProAlaProAlaProGly 20
13 ATGGCTCCCTGAGCCACGCCCTGGCTCCCTCTTATATCCGACCCCTCTCAAGC 72

QY	21	LeuNHrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlyArgLeu	40
Db	73	CTCACTGGCAACCTGCTGCTCACTGCTGCTTCTGATGCTGTTCATCCCAAGCTTG	132
QY	41	ProArgMetGlnGlyAspSerProLeuGlyGlySerSerGlyGlyAspAspProLeu	60
Db	133	CCCCGGATGACGAGAGATTTCCCTCTGGGAGGAGGCTCTCTTGGGGAAAGATGACCACTG	192
QY	61	GlyGlyGlyAspLeuProSerGlyGlyAspSerProArgGlyGlyAspProGlyGly	80
Db	193	GGCGAGGAGGATCTGGCCAGTGAAGAGATTCCACCCAGAGAGAGATCCACCCGGAAAG	252
QY	81	GlyAspLeuProGlyGlyGlyGlyAspLeuProGlyGlyGlyAspLeuProGlyValIleAspPro	100
Db	253	GAGGATCTACTGGAGAGGAGATCTACTGAGAGAGAGATCTTAACTGAAATTAAAGCTT	312
QY	101	LysSerGlyGlyGlyGlySerLeuLysLeuGlyAspLeuProThrValGluValAspGly	120
Db	313	AAATCAGAAAGAGGGCTCCCTCAAGTTAGAGATCTAACTACTGTTGAGGCTCTCGGA	372
QY	121	AspProGlnGlyProGlnAspAsnAlaHisArgAspLysGlyGlyAspAspGlnSerHis	140
Db	373	GATCTCCAGAACCCCAAGATTAATGCCACAGGAGCAAAAGAGGAGATGACCAAGATCAT	432
QY	141	ThrArgTyrGlyGlyAspProProThrProArgValSerProAlaCysAlaGlyValArgPhe	160
Db	433	TGGGGCTATGAGAGCGAACCCGCTCGGCGCCGGGGTGTCCCAAGCTGCGCGGGCGCTTC	492
QY	161	GlnSerProValAspIleArgProGlnLeuAlaIlePheCysProAlaLeuArgProLeu	180
Db	493	CAGTCTCCGGAGGATATCCGCCCCCAAGCTCGCGCTTCTGCTCCGGCCCTTCGCGCCCTG	552
QY	181	GlyLeuLeuGlyPheGlnLeuProProLeuProGlyLeuArgLeuArgAsnGlyHis	200
Db	553	GAACTCCCTGGGCTTCCAGCTCCGCGCGCTCCAGAACGCGCTCGCGCAACATGGCCAC	612
QY	201	SerValGlnLeuThrLeuProProGlyLysGlyMetAlaLeuGlyProGlyValArgGlyTyr	220
Db	613	AGTGTGCAACCTGACCTTCCTCTCGGGCTAGAGATGGCTCTGGGTCCGGGCGGAGATAC	672
QY	221	ArgAlaLeuGlnLeuHisIleuHisThrGlyValIleArgIleArgProGlySerGlyHisThr	240
Db	673	CGGGCTCTGCAGCTGCATCTGCATCTGGGGGGCTGCAGGTGCTCCGGGTGCGAGACACT	732
QY	241	ValGlyGlyHisArgPheProAlaGlyIleHisValValHisIleuSerThrAlaPheAla	260
Db	733	GTCGAGGGCCACCGTTTCCCTGCGCGAGATCCAGCTGGTTCACCTCAGACCGCGCTTGGC	792
QY	261	ArgValAspGlyAlaLeuGlyValArgProGlyGlyLysLeuAlaValIleuAlaIlePheLeuGly	280
Db	793	AGAGTTGACAGAGGCTTGGGGCGCCCGGAGAGCTTGCGCGTGTGGCGCTTCTGGAG	852
QY	281	GlyGlyProGlyGlyAsnSerAlaTyrGlyGlyGlyLeuLeuSerArgLeuGlyGlyIleAla	300
Db	853	GAGGAGCCCGGAAAGAAACAGTGCCTATGACAGATTGCTGCTCCGCTTGGAAAGAAATCGCT	912
QY	301	GlyGlyGlySerGlyThrGlnValProGlyLysAspIleSerAlaLeuLeuProSerAsp	320
Db	913	GAGGAGGCTCAGAGACTCAGGCTCCAGAGCTGACAAATCTGACCTTCGCTCTGCAC	972
QY	321	PheSerArgTyrPheGlnTyrGlyGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	973	TTTCAGCGGCTACTTCCAAATATGAGAGGGTCTCTGACTACACCGGCTGTGGCCCAAGGTCTC	1032
QY	341	IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer	360
Db	1033	ATCTGGACTGTGTTTAAACAGACAGTATGTGTGATGTCTAAGCGAGCTCCACACCTCTCT	1092
QY	361	AspThrLeuThrProGlyAspSerArgLeuGlnLeuAsnPheAspAlaThrGlyPro	380
Db	1093	GACACCCCTGTGGGAGCTGTGTACTTTCGGCTTACGCTGAACCTTCCAGACGACGAGCTT	1153
QY	381	LeuAsnGlyArgValIleGlyAlaSerPheProAlaGlyValAspSerSerProArgAla	400

DB 1153 TTGAATGGGCGAGTATTGAGGCTCTTCCCTGCTGAGTGAACAGAGTCTTGGGCT 1212
QY 401 AAGAGTProValGlnLeuAsnSerCysLeuValAAGlyAspIleLeuValIphe 420
DB 1213 GCTGAGCCAGTTCACACTGAATTCCTGCTGGCTGGTGAATCATCTAGCCCTGGTTTTT 1272
QY 421 GlyLeuLeuPheAlaValTherSerValAlaPheLeuValGlnMetArgArgGlnIleArg 440
DB 1273 GGCCTCTTTTGTGCTGACCGAGCGTTCCTTGTGACATGAGAAGGACAGACA 1332
QY 441 ArgGlyThrIlyGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
DB 1333 AGGGGACCAAGAGGGGCTGTGAGCTACCCGACGAGAGGTAGCCGAGACTGAGACC 1389
RESULT 9
ABL64779
ID ABL64779 standard; DNA; 1552 BP.
XX
AC ABL64779;
XX
DT 15-MAY-2002 (first entry)
XX
DE Lung cancer related gene sequence SEQ ID NO:3116.
XX
KW Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW cytostatic; gene therapy; antineoplastic; Wilms tumour; adenocarcinoma;
KW gene; ds.
XX
XX OS Homo sapiens.
XX
XX WO200194629-A2.
XX
XX 13-DEC-2001.
XX
XX 30-MAY-2001; 2001WO-US010838.
XX
XX 05-JUN-2000; 2000US-0209473P.
XX 05-JUN-2000; 2000US-0209531P.
XX 18-SEP-2000; 2000US-0233133P.
XX 18-SEP-2000; 2000US-0233617P.
XX 20-SEP-2000; 2000US-0234009P.
XX 20-SEP-2000; 2000US-0234034P.
XX 20-SEP-2000; 2000US-0234052P.
XX 22-SEP-2000; 2000US-0234509P.
XX 22-SEP-2000; 2000US-0234567P.
XX 25-SEP-2000; 2000US-0234923P.
XX 25-SEP-2000; 2000US-0234924P.
XX 25-SEP-2000; 2000US-0235077P.
XX 25-SEP-2000; 2000US-0235082P.
XX 25-SEP-2000; 2000US-0235134P.
XX 25-SEP-2000; 2000US-0235280P.
XX 26-SEP-2000; 2000US-0235637P.
XX 26-SEP-2000; 2000US-0235638P.
XX 27-SEP-2000; 2000US-0235711P.
XX 27-SEP-2000; 2000US-0235720P.
XX 27-SEP-2000; 2000US-0235840P.
XX 27-SEP-2000; 2000US-0235863P.
XX 28-SEP-2000; 2000US-0236028P.
XX 28-SEP-2000; 2000US-0236033P.
XX 28-SEP-2000; 2000US-0236038P.
XX 28-SEP-2000; 2000US-0236039P.
XX 28-SEP-2000; 2000US-0236034P.
XX 28-SEP-2000; 2000US-0236109P.
XX 28-SEP-2000; 2000US-0236111P.
XX 28-SEP-2000; 2000US-0236842P.
XX 29-SEP-2000; 2000US-0236891P.
XX 02-OCT-2000; 2000US-0237172P.
XX 02-OCT-2000; 2000US-0237173P.
XX 02-OCT-2000; 2000US-0237278P.
XX 02-OCT-2000; 2000US-0237294P.
XX 02-OCT-2000; 2000US-0237295P.
XX 02-OCT-2000; 2000US-0237316P.

PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
PA (AVALON PHARM.
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DR, Weaver Z;
XX
XX MPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
XX PT agent to be tested for anti-neoplastic activity, and determining a change
XX PT in expression of a gene of a signature gene set.
XX
XX Claim 1; SEQ ID NO 3116; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
XX CC neoplastic agent. The method involves exposing cells to a chemical agent
XX CC to be tested for anti-neoplastic activity, determining a change in
XX CC expression of at least one gene (I) of a signature gene set, where (I)
XX CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
XX CC to ABL70110), or is at least 95% identical to (S), where a change in
XX CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
XX CC activity and can be used in gene therapy. M1 can be used for screening an
XX CC anti-neoplastic agent, and can be used for producing a product which is
XX CC the data collected with respect to the anti-neoplastic agent as a result
XX CC of M1, and the data is sufficient to convey the chemical structure and/or
XX CC properties of the agent. M1 can be used in the treatment of cancer such
XX CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
XX CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
XX CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
XX CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
XX CC tumour
XX
XX SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
XX
XX
XX Alignment Scores:
XX Pred. No.: 1,656-130 Length: 1552
XX Score: 2424.00 Matches: 459
XX Percent Similarity: 100.00% Conservative: 0
XX Best Local Similarity: 100.00% Mismatches: 0
XX Query Match: 100.00% Indels: 0
XX DB: 6 Gaps: 0
XX
XX US-09-967-237A-2 (1-459) x ABL64779 (1-1552)
QY 1 MetaIaProLeuCySPSerProTrieuProLeuLeuIleProAlaProAlaProGly 20
DB 43 ATGGCTCCCTGTGCCCCAGCCCTGCTCCTGTGATCCGCGCCCTGCTCCAGGC 102
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlyArgLeu 40
DB 103 CTCACGTGCAACTGCTGCTGTCTGTGATGCTGTTCATCCACAGAGTTG 162
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerGlyGlyGluAspAspProLeu 60
DB 163 CCCCGATGCAAGAGATTCCTCCCTTGGAGAGAGGCTTTCTGGAGAGATGACCCACTG 222
QY 61 GlyGluGluAspLeuProSerGlyGluGluAspSerProArgGlyGluAspProProGlyGlu 80
DB 223 GCGCGAGAGATCTGCCAGTGAAGAGATTCAACCGAGAGAGATCCACCGGAGAG 282
QY 81 GluAspLeuProGlyGlyGluGluAspLeuProGlyGlyGluGluAspLeuProGlyValIlyPro 100
DB 283 GAGGATCTAAGAGAGAGAGATCTTACCTGAGAGAGAGATCTAAGATTAAGCTT 342
QY 101 LysSerGlyGluGlyGlySerLeuLeuLeuGluAspLeuProThrValGluAlaProGly 120


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Db      343 AATACAGAGAAGAGGCTCCCTGAGTGAAGAGTCACTACTGTTGAGGCTCTGGA 402
Qy      121 ASPProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db      403 GATCTCAAGAAACCCAGAAATATGCCCCAGGAGCAAGAGGAGATGACCAAGATCAT 462
Qy      141 TTPArgTyrGlyGlyAspProProTyrProTyrArgValSerProAlaCysAlaGlyArgPhe 160
Db      463 TGGGCTATGAGAGCGACCGCCCTGGCCCGGGGTGTCCCAAGCTCGCGGGCCGCTTC 522
Qy      161 GlnSerProValAspPheArgProGlnLeuAlaIlePheCysProAlaLeuArgProLeu 180
Db      523 CAGTCCCGGTGGATATCCGCCCACTCGCCCTTCTGCCCCGCGCCCTGCGCCCTCG 582
Qy      181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlyHis 200
Db      583 GAATCTCTGGGCTTCCAGCTCCGCCCTCCCAAACTGGCCCTGGCCCAAAAGGCCAC 642
Qy      201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGluTyr 220
Db      643 AGTGTCAACTGACCTCGCTCCCTGGGCTAGAGATGCTCGGCTCGGGCCGAGAGTAC 702
Qy      221 ArgAlaLeuGlnLeuHisIleuHisTyrGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db      703 CGGCTGTGAGCTGCACTGCACTGGAGGGCTGCAAGTGTCTCGGGCTCGAGACACT 762
Qy      241 ValGlnGlyHisArgPheProAlaGluIleHisValAlaHisIleuSerThrAlaPheAla 260
Db      763 GTGGAAGGCCACCTTCCCTCCCGAGATCCAGTGTTCACCTCAACACACGCTTTGCC 822
Qy      261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db      823 AGAGTTACAGAGGCTTGGGGCGCCCGAGGCTGCGCGCTTGGCGCTTCTTGAG 882
Qy      281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGluIleAla 300
Db      883 GAGGGCCCGAAGAAACAGTCTATGAGAGTGTCTGTCTTGGTGAAGAAATGCT 942
Qy      301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db      943 GAGGAAGCTCAAGAGACTGAGTCCAGAGCTGCAACATCTGCACCTCGCCCTTGAC 1002
Qy      321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db      1003 TTCAGCCGTAATCCATATGAGGGGTCTCTGACTACCCGCTTGGCCAGGGGTGC 1062
Qy      341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaIleGlnLeuHisIleThrLeuSer 360
Db      1063 ATCTGACGTGTATTAAACAGACAGTATGCTGATGCTAAGCAGCTTCACACCTCTCT 1122
Qy      361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db      1123 GACACCTGTGGGGAAGCTGGGACTCTCGGCTACAGTGAACCTTCGAGGAGGACACCT 1182
Qy      381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db      1183 TTGATATGGGAGATGAGTGAAGGCTCTCTCTCTCTGAGTGAAGGACAGCTCTCGGCT 1242
Qy      401 AlAGluProValGlnLeuAsnSerCysLeuAlaIleGlyAspIleLeuAlaLeuValPhe 420
Db      1243 GCTGAGCAATCCAGCTGAATTTCTGCTGGCTGCTCTGTATCTCAAGCCCTGGTTTTT 1302
Qy      421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db      1303 GGCCTCTTTTGTGTGCACAGAGTGCAGCTTCTTGTGCAAGATGAGAGAGGACAGACA 1362
Qy      441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db      1363 AGGGGAACAAAGGGGTGTGACTACCGCCACAGAGGTAGCGAGACTGGAGCC 1419

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XX      XX ABL62179;
AC      15-MAY-2002 (first entry)
XX      DE Colon adenocarcinoma related gene sequence SEQ ID NO: 516.
XX      KM Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
KW      stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;
KW      cytotoxic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;
XX      gene; ds.
OS      Homo sapiens.
XX      WO200194629-A2.
XX      PD 13-DEC-2001.
XX      PF 30-MAY-2001; 2001WO-US010838.
XX      PR 05-JUN-2000; 2000US-0209473P.
XX      PR 05-JUN-2000; 2000US-0209531P.
XX      PR 18-SEP-2000; 2000US-0233133P.
XX      PR 18-SEP-2000; 2000US-0233617P.
XX      PR 20-SEP-2000; 2000US-0234009P.
XX      PR 20-SEP-2000; 2000US-0234034P.
XX      PR 20-SEP-2000; 2000US-0234052P.
XX      PR 22-SEP-2000; 2000US-0234509P.
XX      PR 22-SEP-2000; 2000US-0234567P.
XX      PR 25-SEP-2000; 2000US-0234923P.
XX      PR 25-SEP-2000; 2000US-0234924P.
XX      PR 25-SEP-2000; 2000US-0235077P.
XX      PR 25-SEP-2000; 2000US-0235082P.
XX      PR 25-SEP-2000; 2000US-0235134P.
XX      PR 25-SEP-2000; 2000US-0235280P.
XX      PR 26-SEP-2000; 2000US-0235637P.
XX      PR 26-SEP-2000; 2000US-0235638P.
XX      PR 27-SEP-2000; 2000US-0235711P.
XX      PR 27-SEP-2000; 2000US-0235720P.
XX      PR 27-SEP-2000; 2000US-0235840P.
XX      PR 27-SEP-2000; 2000US-0235863P.
XX      PR 28-SEP-2000; 2000US-0236028P.
XX      PR 28-SEP-2000; 2000US-0236032P.
XX      PR 28-SEP-2000; 2000US-0236033P.
XX      PR 28-SEP-2000; 2000US-0236034P.
XX      PR 28-SEP-2000; 2000US-0236109P.
XX      PR 28-SEP-2000; 2000US-0236111P.
XX      PR 29-SEP-2000; 2000US-0236842P.
XX      PR 29-SEP-2000; 2000US-0236891P.
XX      PR 02-OCT-2000; 2000US-0237172P.
XX      PR 02-OCT-2000; 2000US-0237173P.
XX      PR 02-OCT-2000; 2000US-0237278P.
XX      PR 02-OCT-2000; 2000US-0237294P.
XX      PR 02-OCT-2000; 2000US-0237295P.
XX      PR 02-OCT-2000; 2000US-0237316P.
XX      PR 03-OCT-2000; 2000US-0237425P.
XX      PR 03-OCT-2000; 2000US-0237598P.
XX      PR 03-OCT-2000; 2000US-0237604P.
XX      PR 03-OCT-2000; 2000US-0237606P.
XX      PR 03-OCT-2000; 2000US-0237608P.
XX      PR 03-OCT-2000; 2000US-0237609P.
XX      PR 01-NOV-2000; 2000US-0244867P.
XX      PR 01-NOV-2000; 2000US-0245084P.
XX      PA (AVAL-) AVALON PHARM.
XX      PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI      Soppe DR, Weaver Z;
XX      DR WPI; 2002-188264/24.
XX      PT Screening for anti-neoplastic agent involves exposing cells to a chemical
PT      agent to be tested for anti-neoplastic activity, and determining a change
PT      in expression of a gene of a signature gene set.

```

XX Claim 1; SEQ ID NO 516; 44pp; English.

CC The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour

XX Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

XX

Alignment Scores:

Pred. No.:	1.65e-130	Length:	1552
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

US-09-967-237A-2 (1-459) x ABL62179 (1-1552)

QY 1 MetAlaProLeuCyProSerProTrLeuProLeuLeuIleProAlaProAlaProGly 20

DB 43 ATGCTCTCCCTGTGCCCCAGGCCCTGCTCTCTGATGCCGCGCCCTGCTCAAGC 102

QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40

DB 103 CTCACGTGCAACGTCTCTGCTGCTGCTTCTGATGCTGCTTCATCCCAAGGTTG 162

QY 41 ProArgMetGlnIuAspSerProLeuGlyGlySerSerGlyIuAspAspProLeu 60

DB 163 CCCCAGATGCAAGAGATTCCCTTGGAGAGAGCTTTCTGGGAGAGAGACCACTG 222

QY 61 GlyIuGluAspLeuProSerGlyIuAspSerProArgGlyIuAspProGlyIu 80

DB 223 GCGCAGAGAGATGCTGCCAGTGAAGAGATTCAACCAGAGAGAGATCCACCGAGAG 282

QY 81 GluAspLeuProGlyIuGluAspLeuProGlyIuGluAspLeuProGlyIuValIlePro 100

DB 283 GAGATCTACTCTGAGAGAGAGATCTACTGAGAGAGATCTACTGAAATTAAAGCT 342

QY 101 LysSerGlnGluGlnGlySerLeuIleuGluAspLeuProTrnValIuAlaProGly 120

DB 343 AAATCAGAGAGAGAGGCTCTCTGAAATTAGAGATCTACTACTGTTGAGGCTCTGGA 402

QY 121 AspProGlnIuProGlnIuAsnAsnAlaHisArgAspIleGlyIuAspAspGlnSerHis 140

DB 403 GATCTCTCAAGAACCCAGAAATTAATGCCACAGAGGCAAAAGAGAGATGACAGAGTCA 462

QY 141 ThrArgTrpGlyIuAspProProTrnProArgValSerProAlaCysAlaGlyIuArgPhe 160

DB 463 TGGGCTATGAGAGGAGCCGCTGCGCGGGGTGTCCCAAGCTGTGGCGGGGCTTC 522

QY 161 GlnSerProValAspIleArgProGlnIuLeuAlaIlePheCysProAlaLeuArgProLeu 180

DB 523 CAGTCCCGCGGTGATATCCGCCAGCTCGCGCTTCTCTGCGCGGCTCTGCGCGCTG 582

QY 181 GluLeuLeuGlyPheGlnIleuProProLeuProGlyIuLeuArgLeuArgAsnArgIleHis 200

DB 583 GAATCTCTGAGGCTTCAAGCTCCGCGCTCCAGAACTGCGCTGCGCAAAATGGCCAC 642

QY 201 SerValGlnLeuThrLeuProProGlyIleuGluMetAlaLeuGlyProGlyArgGlyTrp 220

DB 643 AGTGTCACTGACCTCTGCTCTGCGCTAGAGATGCTCTGCGGCCGAGAGATC 702

QY 221 ArgAlaLeuGlnLeuHisIleuHisIleProGlyValAlaIleArgProGlySerGlyHisThr 240

DB 703 CGGGCTGTGACGTGATCTCTCACTGGGGGGCTGACAGGTCTGCGGGCTCGAGACACT 762

QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisIleValIleIleLeuSerThrAlaPheIle 260

DB 763 GTGAAAGCCACCGTTTCCCTGCGGAATTCACGTGTTCACCTCAGACCGCTTTGGC 822

QY 261 ArgValAspGlnAlaLeuGlyArgProGlyIleuAlaValIleuAlaIlePheLeuGln 280

DB 823 AGAGTTGACAGGCTCTGGGCGCGCCGAGAGGCTGCGCGCTTTGCGCTTGTGAG 882

QY 281 GluGlyProGlnIuAsnSerAlaTyGlnIuLeuLeuSerArgLeuGlnIuIleAla 300

DB 883 GAGGGCCCGAAGAAAACAGTGCCTATGAGCAGTTGCTGCTCGCTTGGAAATCGCT 942

QY 301 GluGlnGlySerGlnTrnGlnValProGlyIleuAspIleSerAlaLeuLeuProSerAsp 320

DB 943 GAGAAAGCTCAGAGACTCAGTCCAGAGACTGAGACATATGTGACTCTGCTTGTGAC 1002

QY 321 PheSerArgTrpPheGlnTrpGlyIuSerLeuThrTrnProProCysAlaGlnGlyVal 340

DB 1003 TTCAGCGCTTCTTCCATATAGAGGCTCTTGTGCTACCGCCCTGTGCGAGGGTTC 1062

QY 341 IleTrpThrValPheAsnGlnTrnValMetLeuSerAlaIleGlnLeuHisIleThrLeuSer 360

DB 1063 ATCTGACTGTGTTTAAACACAGACAGTATGCTGATGCTAGCTAGCAGCTTCAACACCTCTCT 1122

QY 361 AspThrLeuTrpGlyIuProGlyIuAspSerArgLeuGlnIleuAsnPheAlaThrGlnPro 380

DB 1123 GACACCTGTGGGAGCTGTGACTCTCGGTTCAGCTTGAAGCTTCCAGACCAAGCT 1182

QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValIleAspSerProArgAla 400

DB 1183 TTGAATGGCGAGATTTGAGGCTCTTCTCTCTGAGTGGACAGCAATCTCGGCT 1242

QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaIleAspIleLeuAlaIleValPhe 420

DB 1243 GCTAGGCAAGTCCAGTGAATTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302

QY 421 GlyLeuLeuPheAlaValTrnSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440

DB 1303 GGCCTCTTTTGTCTGTCACCAAGCGTGCCTTCTGTGCAAGATGAGAGACACACAGA 1362

QY 441 ArgGlyThrIleGlyIuValIleSerTyArgProAlaGluValAlaGluThrGlyAla 459

DB 1363 AGGGAAACAAAGGGGTGTGAGCTACCGCCAGACAGATGAGCTGAGAGCC 1419

RESULT 11

ABL65416

ID ABL65416 standard; DNA; 1552 BP.

XX ABL65416;

AC 15-MAY-2002 (first entry)

XX

DE Lung cancer related gene sequence SEQ ID NO:3753.

XX

XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;

XX stomach; lung; prostate; pancreas; carcinoma; antitumour; cancerous;

XX cytostatic; gene therapy; antineoplastic; Wilms' tumour; adenocarcinoma;

XX gene; ds.

XX OS Homo sapiens.

XX

XX WO200194629-A2.

XX

XX 13-DEC-2001.

XX

PF 30-MAY-2001; 2001WO-US010838.
XX
XX 05-JUN-2000; 2000US-0209473P.
PR 05-JUN-2000; 2000US-0209531P.
PR 18-SEP-2000; 2000US-0233133P.
PR 18-SEP-2000; 2000US-0233617P.
PR 20-SEP-2000; 2000US-0234009P.
PR 20-SEP-2000; 2000US-0234034P.
PR 20-SEP-2000; 2000US-0234052P.
PR 22-SEP-2000; 2000US-0234509P.
PR 22-SEP-2000; 2000US-0234577P.
PR 25-SEP-2000; 2000US-0234923P.
PR 25-SEP-2000; 2000US-0234924P.
PR 25-SEP-2000; 2000US-0235077P.
PR 25-SEP-2000; 2000US-0235082P.
PR 25-SEP-2000; 2000US-0235134P.
PR 25-SEP-2000; 2000US-0235280P.
PR 26-SEP-2000; 2000US-0235637P.
PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
PA (AVAL-) AVALON PHARM.
XX
XX
PI Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppe DK, Weaver Z;
XX
XX WPI; 2002-188264/24.
XX
XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PT in expression of a gene of a signature gene set.
XX
XX
XX Claim 1; SEQ ID NO 3753; 44pp; English.
XX
XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (1)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytosolic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC the data collected with respect to the anti-neoplastic agent as a result
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous

CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms
CC tumour
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
Alignment Scores:
Pred. No.: 1.65e-130 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 6 Gaps: 0
US-09-967-237A-2 (1-459) x ABL65416 (1-1552)
QY 1 MetAlaProLeuCySerProSerProTProLeuProLeuLeuIleProAlaProAlaProGly 20
DB 43 ATGGCTCCCTGCTGCCCCAGCCCTGGCTCCCTCTTATCCCGCCCTGCTCCAGGC 102
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 103 CTCACTGTGAATGCTGTGCTGCTCACTGCTGCTTCTGATGCTGTCCATCCCGAGAGTTG 162
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB 163 CCCCGATGAGAGGATTCCTCCCTGGAGAGGCTCTTCTGGGAAATGATGACCATG 222
QY 61 GLYGLUGLUAAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 223 GCGGAGAGGATTCGCCAGTGAAGAGATTCAACCCAGAGAGAGATCAACCCGAGAG 282
QY 81 GluAspLeuProGlyGlyGluGluAspLeuProGlyGlyGluGluAspLeuProGlyValIysPro 100
DB 223 GCGGAGAGGATTCGCCAGTGAAGAGATTCAACCCAGAGAGAGATCAACCCGAGAG 282
QY 81 LysSerGluGluGluGlySerLeuGlyLeuGluAspLeuProThrValGluAlaProGly 120
DB 283 GAGGATCTACCTGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAATTAAAGCTT 342
QY 101 LysSerGluGluGluGlySerLeuGlyLeuGluAspLeuProThrValGluAlaProGly 120
DB 343 AAATCAGAAAGAGAGGCTCCCTGAAGTGAAGATCTACCTGTTAGGCTCTGGA 402
QY 121 AspProGlnGluProGlnAsnAsnAlaHisAspAspLysGluGlyAspAspGlnSerHis 140
DB 403 GATCCTCAAGAACCCCGAATAATGCCCAAGAGAAAGAGGATCAACCAAGATCAT 462
QY 141 TrpArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
DB 463 TGGCGCTATGAGAGGACCCGCCCTGCGCCGAGTGTCCCAAGCTGCCGCGGCCCTTC 522
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 523 CAGTCCCGGTGATATCCGCCCCCGCCAGCTCGCGGCTTGTGCCGCCCTGCGGCCCTG 582
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluProGluArgGluAsnGlyHis 200
DB 583 GAATCTCTGGGCTTCAGATCCCGCGCTCCCAAGATCTCGCTGGCAATGCGCCAG 642
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
DB 643 AGTGTCAACTGACCTTCCTGCTGCTGAGATGCTGAGTCCCGGCGGAGTAC 702
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrrProGlyAlaAlaGlyArgProGlySerGlnHisTrr 240
DB 703 CGGCGCTCAGTGTGATGTGACGTGGGGGCTGCGAGGTGTCGGGCTCGAGACACT 762
QY 241 ValGlnGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
DB 763 GTGGAAGGCCACCGTTTCCCTGCCAGATCCAGTGTCACTCAGACACCGCTTGGC 822
QY 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
DB 823 AGAGTTGAGAGGCTTGGGGCGCCCGGAGGCTGTGGCTGTGGCCCTTTCGGAG 882
QY 281 GluGlyProGluGluAsnSerLysTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300

Db 883 GAGGCCCGGAGAAAAACAGTCTATGACAGTTCCTGCTCGTGGAGAAATCGCT 942
Qy 301 GUGUGUGYserGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGGCTCAGACCTCAGGTCCAGACATATGACATCTGCTCCCTGAC 1002
Qy 321 PheSerArgIYrPheGlnIYrGluYserLeuThrProProCysAlaGlnIYrVal 340
Db 1003 TTCACCCCTACTTCCATATATAGGGGCTCTGACTACACCCCTGTCGAGGGTTC 1062
Qy 341 ILeTPThrValPheAsnGlnThrValMetLeuSerAlaYseGlnLeuHisThrLeuSer 360
Db 1063 ATCTGAGCTGTGTTTAAACAGACAGTGAATGCTGAGGTAAACAGCTCCACACCTCTCT 1122
Qy 361 AspThrLeuTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCCGTGGGAGCTGTGACTCTCGCTACAGCTGAACCTCCAGACGAGAGCT 1182
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1183 TTGAATGGGCGCATGATAGAGGCTCTTCCCTGCTGAGTGAAGACAGCTCTGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCCAGTCCACACTGAATTCCTGCTGCTGCTGAGCATCTAGCCCTGGTTTTT 1302
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCTCTTTTGTGCTGTCACCGCGTCCGCTTCTTGACATAGAGAGGACAGACAGA 1362
Qy 441 ArgGlyThrIYrGlyGlyValSerIYrArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGAGACCAAGGGGCTGTGACTACCCGCCAGACAGGTAGCCGAGACTGAGACC 1419

RESULT 12
ABL68346
ID ABL68346 standard; DNA; 1552 BP.

XX ABL68346;

XX AC 15-MAY-2002 (first entry)

XX DT 15-MAY-2002 (first entry)

XX DE Kidney cancer related gene sequence SEQ ID NO: 6683.

XX XX Human; cancer; colon; breast; ovary; oesophagus; kidney; thyroid;
stomach; lung; prostate; pancreas; carcinoma; antitumor; cancerous;
cytostatic; gene therapy; antineoplastic; Wilms' tumor; adenocarcinoma;
gene; ds.

XX XX Homo sapiens.

XX OS WO200194629-A2.

XX PD 13-DEC-2001.

XX PF 30-MAY-2001; 2001WO-US010838.

XX XX 05-JUN-2000; 2000US-0209473P.

XX PR 05-JUN-2000; 2000US-0209531P.

XX PR 18-SEP-2000; 2000US-0231133P.

XX PR 18-SEP-2000; 2000US-0231617P.

XX PR 20-SEP-2000; 2000US-0234009P.

XX PR 20-SEP-2000; 2000US-0234034P.

XX PR 20-SEP-2000; 2000US-0234052P.

XX PR 22-SEP-2000; 2000US-0234509P.

XX PR 22-SEP-2000; 2000US-0234567P.

XX PR 25-SEP-2000; 2000US-0234923P.

XX PR 25-SEP-2000; 2000US-0235077P.

XX PR 25-SEP-2000; 2000US-0235082P.

XX PR 25-SEP-2000; 2000US-0235134P.

XX PR 25-SEP-2000; 2000US-0235280P.

XX PR 26-SEP-2000; 2000US-0235637P.

PR 26-SEP-2000; 2000US-0235638P.
PR 27-SEP-2000; 2000US-0235711P.
PR 27-SEP-2000; 2000US-0235720P.
PR 27-SEP-2000; 2000US-0235840P.
PR 27-SEP-2000; 2000US-0235863P.
PR 28-SEP-2000; 2000US-0236028P.
PR 28-SEP-2000; 2000US-0236032P.
PR 28-SEP-2000; 2000US-0236033P.
PR 28-SEP-2000; 2000US-0236034P.
PR 28-SEP-2000; 2000US-0236109P.
PR 28-SEP-2000; 2000US-0236111P.
PR 29-SEP-2000; 2000US-0236842P.
PR 29-SEP-2000; 2000US-0236891P.
PR 02-OCT-2000; 2000US-0237172P.
PR 02-OCT-2000; 2000US-0237173P.
PR 02-OCT-2000; 2000US-0237278P.
PR 02-OCT-2000; 2000US-0237294P.
PR 02-OCT-2000; 2000US-0237295P.
PR 02-OCT-2000; 2000US-0237316P.
PR 03-OCT-2000; 2000US-0237425P.
PR 03-OCT-2000; 2000US-0237598P.
PR 03-OCT-2000; 2000US-0237604P.
PR 03-OCT-2000; 2000US-0237606P.
PR 03-OCT-2000; 2000US-0237608P.
PR 01-NOV-2000; 2000US-0244867P.
PR 01-NOV-2000; 2000US-0245084P.
XX (AVAIL-) AVALON PHARM.
XX PA
XX Young PE, Augustus M, Carter KC, Ebner R, Endress G, Horrigan S;
PI Soppet DR, Weaver Z;
XX MPI: 2002-188264/24.
XX DR

XX Screening for anti-neoplastic agent involves exposing cells to a chemical
PT agent to be tested for anti-neoplastic activity, and determining a change
PR in expression of a gene of a signature gene set.
XX

XX Claim 1; SEQ ID NO 6683; 44pp; English.

XX The present invention describes a method (M1) for screening for an anti-
CC neoplastic agent. The method involves exposing cells to a chemical agent
CC to be tested for anti-neoplastic activity, determining a change in
CC expression of at least one gene (I) of a signature gene set, where (I)
CC comprises a sequence (S) selected from 8447 sequences (given in ABL61664
CC to ABL70110), or is at least 95% identical to (S), where a change in
CC expression is indicative of anti-neoplastic activity. (I) has cytostatic
CC activity and can be used in gene therapy. M1 can be used for screening an
CC anti-neoplastic agent, and can be used for producing a product which is
CC of M1, and the data is sufficient to convey the chemical structure and/or
CC properties of the agent. M1 can be used in the treatment of cancer such
CC as colon, breast, stomach, lung, thyroid, oesophageal, ovarian, kidney,
CC prostate or pancreatic cancer, adenocarcinoma, carcinoma, clear cell
CC cancer, infiltrating ductal cancer, infiltrating lobular cancer, squamous
CC cell carcinoma, neuroendocrine carcinoma, papillary carcinoma and Wilms'
CC tumour

XX SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

XX Alignment Scores:

Pred. No.:	1,65e-130	Length:	1552
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	6	Gaps:	0

XX US-09-967-237A-2 (1-459) x ABL68346 (1-1552)

Qy 1 MetAlaProLeuGysProSerProTyrPheuProLeuLeuIleProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGCTCCAGCCCTGCTCTCTGTGATGATCCGGGCTGCTCCAGGC 102

QY	21	LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnIleuLeu	40
Db	103	CTCACTGTGCAACTCTCTGCTCACTGCTGCTTGAATGCTGTCCATCCCAAGAGTTG	162
QY	41	ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu	60
Db	163	CCCCGGATGACGAGAGATTCCCCCTTGGGAGGAGGCTCTTGGGGAAAGATGACCACTG	222
QY	61	GlyGlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu	80
Db	223	GGCGGAGGAGACTCTCCAGTAAAGATTACCAAGAGAGAGAAATCCACCCGAGAG	282
QY	81	GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValIlyspPro	100
Db	283	GAGGATCTAACCCTGGAGAGAGGATCTAACCCTGGAGAGAGAGATCTAACCCTGAATTAAGCT	342
QY	101	LysSerGlyGluGlyGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly	120
Db	343	AAATCAGAAAGAGAGGCTCCCTGAAAGTTAGAGATCTAACCCTGTTGAGGCTCTCGGA	402
QY	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis	140
Db	403	GATCTCAAGAAACCCACAGATATATCCACAGAGACAAAGAGGGGAAATGACCAAGATCAT	462
QY	141	TrpArgIleGlyGlyAspProProThrProArgValSerProAlaCysAlaGlyArgPhe	160
Db	463	TGGCGCTATGAGAGCGACCCGCGCTTGCGCCGGAGTGTCCCAAGCTGGCGGGCGGCTTC	522
QY	161	GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu	180
Db	523	CAGTCCCGGAGGATATCCGCCCCAGCTCGCGGCTTGTGCGGAGCTGTGGCCCCCTG	582
QY	181	GluLeuLeuGlyPheGluLeuProProLeuProGluLeuArgLeuArgAsnAsnIlyHis	200
Db	583	GAACTCCTGGGCTTCAGCTCCCCGCGCTCCAGAAATCGGCTCGCAACAATGGCCAC	642
QY	201	SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyValArgGluTyr	220
Db	643	AGTGTGCAACTGACCCCTGCTCTGGGCTAGAGATGAGTGTCTGGTGCCTGGGCGGAGATAC	702
QY	221	ArgAlaLeuGlnLeuHisIleuHisIleProGlyAlaAlaArgValArgProGlySerGluHisIleThr	240
Db	703	CGGGCTCTGCACTCAATGTGACTTGGGGGGGTGGAGATCGTCCGGAGCTCGGAGCAACT	762
QY	241	ValGluGlyHisArgPheProAlaGluIleHisValIleHisLeuSerThrAlaPheAla	260
Db	763	GTGGAAAGCCACCGTTCCCTGCTCCGAGATCCAGTGATTCACTCAGCACCGCTTTGGC	822
QY	261	ArgValaAspGluAlaLeuGlyValArgProGlyGlyLeuAlaValaLeuAlaAlaPheLeuGlu	280
Db	823	AGAGTTGACGAGGCTTGGGGGGCGCCGGAGGCTGTGGCTGTGGCTTCTTGTGAAG	882
QY	281	GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla	300
Db	883	GAGGGCCCCGGAAGAAACAAGTCCCTATGACAGATTGCTCTCGCTTGGAGAAATCGCT	942
QY	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	943	GAGGAAAGCTCAGAAACTCAGGTCCCAAGACTGAGCATATCTGCACTCCCTGCTTGAC	1002
QY	321	PheSerArgTyrPheGlnTyrGluGlySerLeuThrProProCysAlaGlnGlyVal	340
Db	1003	TTCACCGCTCACTTCCAAATATGAGGGGTCTCTGACTCAACGCGCTGTGGCCAGGGGTTC	1062
QY	341	IleThrIleThrValPheAsnGlnThrValIleCysSerAlaLysGlnLeuHisIleThrLeuSer	360
Db	1063	ATCTGGACTGTGTTTAACCAAGACAGTATGTGAGTGTGAAGCACTCCACACCTCTCT	1122
QY	361	AspThrLeuThrGlyValProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
Db	1123	GACACCCCTGTGGGGACCTGTGTGACTCTCGGCTACAGCTGAACCTTCGAGCGACGCACT	1182

OY		38L	neunsnngiaagvAl11legluAalasePhProhlaaIyValapseserProrxALA	400
Dd		1183	TtgaatggcGAGATtTGAAGCCTCTTCCTCGCTGAGATGACAGCAATCTCCGGGCT	1242
OY		401	AlaaguProvalgInleuaenSerCyaleuaAlaIagiAspiileueAlaleuValphe	420
Dd		1243	GCTGAGCCAGCAGCCAGTGAAATTCCTGCCTGCTGCTGTGACAATCTTAGGCCCTGGTTTTT	1302
OY		421	GlyleueuPheAlaValIThrSeValAlaPheleuValGlnmetArGaArgGlnhiARg	440
Dd		1303	GGCCTCCTTTTGTGCTGACCAAGGCTGCGCTCTTThGAGAATGAABAGCACAGACAAGA	1362
OY		441	ArgglyThrlysgIgyIyValserTyArArgProhlaaIuValAlaagiurhgIyala	459
Dd		1363	AGGGGAACCAAGGGGGGTGTGACTTACCGCCAGCAGAGTAGCCGACCTGGAGCC	1419
RESULT 13				
ABX76385				
ID	ABX76385	standard; DNA;	1552 BP.	
XX				
AC	ABX76385;			
XX				
DT	02-APR-2003	(first entry)		
XX				
DE	Lung cancer-associated polynucleotide #249.			
XX				
KW	Lung cancer-associated polynucleotide; gene; ds; cytosatic; emphysema;			
KM	antiinflammatory; antistatic; non-small cell lung cancer; atelectasis;			
KW	small cell lung cancer; benign lesion; precancerous lesion; bronchitis;			
KM	chronic obstructive pulmonary disease; hypersensitivity pneumonitis;			
KW	interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.			
OS	Unidentified.			
XX				
XX				
PN	WO200286443-A2.			
PD				
XX	31-OCT-2002.			
PF				
XX	18-APR-2002; 2002WO-US012476.			
PR	18-APR-2001; 2001US-0284770P.			
PR	10-MAY-2001; 2001US-0290492P.			
PR	09-NOV-2001; 2001US-0339245P.			
PR	13-NOV-2001; 2001US-0350666P.			
PR	29-NOV-2001; 2001US-0354370P.			
XX	12-APR-2002; 2002US-0372246P.			
PA	(EOSB-) EOS BIOTECHNOLOGY INC.			
PI	Aziz N, Murray R;			
DR	WPI; 2003-093161/08.			
DR	P-PSDB; ABUS6656.			
PT				
PT	Detecting a lung cancer-associated transcript in a cell from a patient			
PT	for treating lung cancer, by contacting a biological sample from the			
PT	patient with a polynucleotide that exhibits increased or decreased			
PT	expression in lung cancer.			
XX				
XX				
PS	Claim 22; Page 379-380; 453bp; English.			
XX				
CC	The invention relates to a method for detecting a lung cancer-associated			
CC	transcript in a cell from a patient, comprising contacting a biological			
CC	sample from the patient with a polynucleotide that selectively hybridises			
CC	to a sequence that is at least 80 % identical to a gene that exhibits			
CC	increased or decreased expression in lung cancer samples. Lung cancer-			
CC	-associated polynucleotides and polypeptides are used for identifying a			
CC	compound that modulates a lung cancer-associated polypeptide, for			
CC	inhibiting proliferation of a lung cancer-associated cell to treat lung			
CC	cancer in a patient and for treating a mammal having lung cancer by			
CC	administering a modulatory compound identified. The methods are useful			
CC	for treating lung cancer, such as small cell lung cancer, non-small cell			
CC	lung cancer or other benign or precancerous lesions, e.g. atelectasis,			
CC				

CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC ABX76124-ABX76474 represent lung cancer-associated polynucleotides of the
CC invention

XX Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;

Alignment Scores:

Pred. No.:	1-65e-130	Length:	1552
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	8	Gaps:	0

US-09-967-237A-2 (1-459) x ABX76385 (1-1552)

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QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACGTGCAACTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 162
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
Db 163 CCCGGAGTGCAGAGAGATTCCCTTGGAGAGAGCTCTTGGGAGATGACCCACCTG 222
QY 61 GlyGluGluAspLeuProSerGlyGluAspSerProArgGluGluAspProGlyGlu 80
Db 223 GCGCAGGAGATCTGCCAGTGAAGAGATTCACCAAGAGAGAGATCCACCGGAGAG 282
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValLysPro 100
Db 283 GAGGATCTAACCTGAGAGAGAGATTTACCTGAGAGAGAGATCTAACCTGAGATTAGCT 342
QY 101 LysSerGlnGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 343 AATACAGAAAGAGAGGCTCCCTGAAATTAGAGATCTACCTGTTGAGGCTCTGGA 402
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspGlyGlyGlyAspAspGlnSerHis 140
Db 403 GATCCTCAAGAACCCCAAGATATATGCCACAGGAGCAAGAGGAGTACCAAGATCAT 462
QY 141 TrpArgTyrGlyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCGCTATGAGAGGAGCCCGCCCTGGCCCGGAGTGTCCCAAGCTTGGCGGCGGCTTC 522
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCGGGTGGATATCCGCCCCCAGCTCCGCGCTTCTGCGCGCCCTGCGCCCTG 582
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuAlaGluArgAsnArgHis 200
Db 583 GAACCTCCTGGGCTTCCACCTCCGCGCTCCAGAACTGCGCTGCGCAACATATGGCCAC 642
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyValArgLys 220
Db 643 AGTGTGCAACTGACCTTCCCTGCTGAGGCTTGAAGATGGCTTGGGTCCTCGGAGGAGTAC 702
QY 221 ArgAlaLeuGlnLeuHisLeuHisArgTyrGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 703 CGGGCTATGAGAGCTCATCTGACTGGGGGGCTGCAAGGCGTCCGGGGTCCGAGACACT 762
QY 241 ValGluGlyHisArgPheProAlaGluLysHisValValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCAACCGTTTCCCTGCCAGATCCACGAGGTTCACCTTGACACCGCCCTTTC 822
QY 261 ArgValaAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280

Db 823 AGAGTTAGCAGAGGCTTGGGCGCCCGGAGAGGCTGGCGGTGGCCGCTTCTGGAG 882
QY 281 GluGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGluLysAla 300
Db 883 GAGGCGCCGAGAAACACAGTCTATAGCATGAGTGTGCTGTGCTTGGAAAGAAATCCCT 942
QY 301 GluGluGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAGGCTCAGAGACTCAGGTCCCGAGACTGAGCATATCTGACTCTGCTCTTAC 1002
QY 321 PheSerArgTyrPheGlnTyrGlyGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAAGCGCTACTCTTCATATAGAGGGGTCTGACTACACCGCCCTGAGCCAGGGTGC 1062
QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1063 ATCTGACTGTGTTTAAACAGACAGTGAATGCTGAGTCTTAAGCAGCTTCACACCTCTCT 1122
QY 361 AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCTGTGGAGACCTGTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1182
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValaAspSerSerProArgAla 400
Db 1183 TTGAATGGCGCAGATGATGAGGCTCTTCCCTGCTGAGTGAAGACAGCATGCTCGGCT 1242
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuAlaPhe 420
Db 1243 GCTGAGCAGATCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCTCTTTTGTGCTACAGAGTGCCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1362
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValaAlaGluThrGlyAla 459
Db 1363 AGGGAAACCAAGGGGGGTGAGCTACCGCCAGAGAGTAAAGCGAATCAGAGGCC 1419

RESULT 14
ABX76124
ID ABX76124 standard; DNA; 1552 BP.
XX
AC ABX76124;
DT 02-APR-2003 (first entry)
XX
DE Lung cancer-associated polynucleotide #1.
KW Lung cancer-associated polynucleotide; gene; ds; cytosstatic; emphysema;
KW antiinflammatory; antisthmatic; non-small cell lung cancer; atelectasis;
KW small cell lung cancer; benign lesion; precancerous lesion; bronchitis;
KW chronic obstructive pulmonary disease; hypersensitivity pneumonitis;
KW interstitial pulmonary fibrosis; fibrosis; asthma; bronchiectasis.
OS Unidentified.
XX
XX WO200286443-A2.
XX
XX 31-OCT-2002.
XX
XX 18-APR-2002; 2002WO-US012476.
XX
XX 18-APR-2001; 2001US-0284770P.
XX
XX 10-MAY-2001; 2001US-0290492P.
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XX 09-NOV-2001; 2001US-0339245P.
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XX 13-NOV-2001; 2001US-0350666P.
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XX 29-NOV-2001; 2001US-0334370P.
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XX 12-APR-2002; 2002US-0372246P.
XX
XX (BOSB-) EOS BIOTECHNOLOGY INC.
XX
XX PA
XX PI Aziz N, Murray R;

XX WPI: 2003-093161/08.
DR P-PSDB; ABUS6408.
XX
PT Detecting a lung cancer-associated transcript in a cell from a patient
PT for treating lung cancer, by contacting a biological sample from the
PT patient with a polynucleotide that exhibits increased or decreased
PT expression in lung cancer.
XX
PS Claim 22; Page 189; 453bp; English.
CC The invention relates to a method for detecting a lung cancer-associated
CC transcript in a cell from a patient, comprising contacting a biological
CC sample from the patient with a polynucleotide that selectively hybridises
CC to a sequence that is at least 80 % identical to a gene that exhibits
CC increased or decreased expression in lung cancer samples. Lung cancer-
CC associated polynucleotides and polypeptides are used for identifying a
CC compound that modulates a lung cancer-associated polypeptide, for
CC inhibiting proliferation of a lung cancer-associated cell to treat lung
CC cancer in a patient and for treating a mammal having lung cancer by
CC administering a modulatory compound identified. The methods are useful
CC for treating lung cancer, such as small cell lung cancer, non-small cell
CC lung cancer or other benign or precancerous lesions, e.g. atelectasis,
CC emphysema, bronchitis, chronic obstructive pulmonary disease, fibrosis,
CC hypersensitivity pneumonitis, interstitial pulmonary fibrosis, asthma and
CC bronchiectasis. The genes, polynucleotides and polypeptides are useful
CC for diagnostic purposes and as targets for screening for therapeutic
CC compounds that modulate lung cancer, such as antibodies. Sequences
CC AXK76124-ABK76474 represent lung cancer-associated polynucleotides of the
CC invention
CC
XX
SQ Sequence 1552 BP; 302 A; 471 C; 461 G; 318 T; 0 U; 0 Other;
XX
Alignment Scores:
Pred. No.: 1 656-130 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0
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QY 1 MetAlaProLeuCyProSerProTrpLeuProLeuLeuProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTCGCCAGCCCTGGCTCCTCTGTGATCCGGCCCTGCTCCAGGC 102
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACGTGTGAACCTGCTGTCTACTGCTGTGATGCTGCTCCATCCCAAGGTTG 162
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyVserSerGlyGluAspAspProLeu 60
Db 163 CCCCAGATGACGAGAGATTCCTCCCTTGGAGAGGCTCTTCTGGAGAGATGACCCACTG 222
QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db 223 GGCAGAGAGATGTGCCAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 282
QY 81 GluAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyValValPro 100
Db 283 GAGATCTTACTGAGAGAGAGATCTACTGAGAGAGAGATCTTGAAGTTAAACCT 342
QY 101 LysSerGlnGluGlnGlySerLeuValLeuGlnAspLeuProThrValGlnAlaProGly 120
Db 343 AATATCAAGAAAGAGGCTCCCTGAATTAAGAGATCTTACTGTTGAGGCTCTCGA 402
QY 121 AspProGlnGluProGlnAsnAlaHisArgAspArgGlnGlyAspAspGlnSerHis 140
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QY 141 TTPATGT 160

Db 463 TGGCGCTATGAGAGCAACCCGCCCTGGCCCCGGGGTGTCCCAAGCTGGCGGGCCGCTTC 522
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Db 523 CAGTCCCGGTGATATCCGCCCCCAAGCTGGCGGCTTCTGGCCCGGCTCCGCCCTTG 582
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnArgHis 200
Db 583 GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGGCAACATATGGCCAC 642
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyTyr 220
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QY 221 ArgAlaLeuGlnLeuHisLeuHisSerTrpGlyValAlaAlaGlyArgProGlySerGlnHisThr 240
Db 703 CGGGCTGTGAGTGCATCTGCATGGGGGGCTGCAGCTGTCTCGGGCTCGAGCACACT 762
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Db 763 GTGGAAGGCCACCGTTTCCCTGCGAGATCCAGTGGTTCACCTCAGACCCGCTTGGCC 822
QY 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTGACGAGGCTTGGGGCCCGGAGGCTGGCGGTGTGGCCGCTTGTGGAG 882
QY 281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
Db 883 GAGGGCCCGGAAGAAACAGTGTCTATGACATTCGTCTGTCTGTGGAGAAATCGCT 942
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Db 943 GAGGAAGGCTCAGAGACTCAGGCTCCAGGACTGAGCATATCTCCTCCTGAC 1002
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCySerAlaGlnIleVal 340
Db 1003 TTCAAGCGCTACTTCCATATGAGGGTCTCTACTACACCGCCCTGTGGCGAGGTGTC 1062
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisThrLeuSer 360
Db 1063 ATCTGACCTGTATTAAACAGACAGTATCTAGTGTCTAAGACGCTCCACACCTCTCT 1122
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCTGTGGGAGACTGGTGTACTCTGGCTCACCTGAACTTCGAGCGACGAGCCT 1182
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1183 TTGAATGGCGAGTGAATGAGGCTCTCTCTCTGTGTGAGTGAACAGCTCTCGGGCT 1242
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCGACATCCAGCTGAATTCCTGCTGGCTGCTGCTGATCCATCCAGCCCTGATT 1302
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCTCTTTTCTGTGACACAGCTCGCGCTTCTCTGTGAGATGAGAGGCGACAGA 1362
QY 441 ArgGlyThrTrpGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
Db 1363 AGGGAAACCAAGAGGGGTGTGAGCTACCGCCAGAGAGGTAGCCAGACTGGAGCC 1419
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ID ADG89343 standard; DNA; 1552 BP.
XX
AC ADG89343;
XX
XX 11-MAR-2004 (first entry)
XX
XX
DE Cancer detection method related gene #6.
KW de; cancer; gene expression;

Db 1363 AGGGGAACCAAGGGGGTGTGACCTACCGCCAGAGAGGTAGCCGAGACTGAGGCC 1419

Search completed: August 19, 2005, 22:26:00
Job time : 785 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2005, 21:34:10 ; Search time 248 Seconds
(without alignments)
3028.432 Million cell updates/sec

Title: US-09-967-237A-2
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6 : /cgn2_6/prodata/1/ina/bacfillseq.seq:
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed and is derived by analysis of the total score distribution.

SUMMARIES

Result	No.	Score	Query Match	Length	DB	ID	Description
1	2424	100.0	1522	2	US-08-481-558B-1	Sequence 1, Appl1	
2	2424	100.0	1522	2	US-08-477-504A-1	Sequence 1, Appl1	
3	2424	100.0	1522	2	US-08-466-756A-1	Sequence 1, Appl1	
4	2424	100.0	1522	2	US-08-485-662B-1	Sequence 1, Appl1	
5	2424	100.0	1522	3	US-08-787-739-1	Sequence 1, Appl1	
6	2424	100.0	1522	3	US-08-487-077A-1	Sequence 1, Appl1	
7	2424	100.0	1522	3	US-08-485-663A-1	Sequence 1, Appl1	
8	2424	100.0	1522	3	US-08-485-749D-1	Sequence 1, Appl1	
9	2424	100.0	1522	3	US-09-178-115-1	Sequence 1, Appl1	
10	2424	100.0	1522	3	US-09-177-776-1	Sequence 1, Appl1	
11	2424	100.0	1522	4	US-09-772-119B-1	Sequence 1, Appl1	
12	2424	100.0	1522	4	US-08-260-190-5	Sequence 5, Appl1	

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14	2420	99.8	1552	4	US-09-949-016-3332	Sequence 4332, Appl
15	2233	92.1	15052	4	US-08-260-190-23	Sequence 23, Appl
16	2227	91.9	1389	3	US-08-333-169-1	Sequence 1, Appl
17	2227	91.9	1399	4	US-08-260-190-1	Sequence 1, Appl
18	2036	84.0	1397	1	US-07-964-589-1	Sequence 1, Appl
19	2036	84.0	1397	5	PCR-US93-02024-1	Sequence 1, Appl
20	1253.5	51.7	11237	4	US-09-949-016-11913	Sequence 11913, A
21	1253.5	51.7	11237	4	US-09-949-016-16074	Sequence 16074, A
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31	1176.5	48.5	10988	3	US-09-177-776-5	Sequence 5, Appl
32	1176.5	48.5	10988	4	US-09-177-776-5	Sequence 5, Appl
33	714	29.5	415	2	US-08-472-719B-5	Sequence 28, Appl
34	714	29.5	415	2	US-08-481-658B-28	Sequence 28, Appl
35	714	29.5	415	2	US-08-477-504A-28	Sequence 28, Appl
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37	714	29.5	415	2	US-08-485-862B-28	Sequence 28, Appl
38	714	29.5	415	3	US-08-487-077A-28	Sequence 28, Appl
39	714	29.5	415	3	US-08-485-863A-28	Sequence 28, Appl
40	714	29.5	415	3	US-08-485-049D-28	Sequence 28, Appl
41	714	29.5	445	3	US-08-787-739-28	Sequence 28, Appl
42	714	29.5	445	3	US-09-178-115-28	Sequence 28, Appl
43	714	29.5	445	3	US-09-177-776-28	Sequence 28, Appl
44	714	29.5	445	4	US-09-772-719B-28	Sequence 28, Appl
45	629	25.9	1401	2	US-08-481-658B-49	Sequence 49, Appl
46	629	25.9	1401	2	US-08-477-504A-49	Sequence 49, Appl

ALIGNMENTS

RESULT 1

US-08-481-658B-1
; Sequence 1, Application US/08481658E
Referred via COFOOT

GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona J. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California

COMPUTER READABLE FORM:
DATE: 05/28/80
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (ZPO)
CURRENT APPLICATION DATA:

1 CLASSIFICATION: 424
2
3 PRIOR APPLICATION DATA:
4 APPLICATION NUMBER: US 08/260,190
5 FILING DATE: 15-JUN-1994
6 ATTORNEY/AGENT INFORMATION:
7 NAME: lauder, leona L.
8 REGISTRATION NUMBER: 30,863
9 REFERENCE/DOCKET NUMBER: D-0021.3
10 TELECOMMUNICATION INFORMATION:
11 TELEPHONE: 415-435-2034
12 TELEFAX: 415-435-0727

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-481-658B-1

Alignment Scores:
Pred. No.: 7,09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
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Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-967-237A-2 (1-459) x US-08-481-658B-1 (1-1522)

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QY 141 TyrArgTyrGlyAspProProTrrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGGAGGCGACCCGCTCGGCGCCCGGGGTGTCCCAAGCTCGCGGGCGGCTTC 492
QY 161 GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGGTGAATCCCGCCCAAGTCGCGCTTGTCCCGGGCCCTGCGCCCTG 552
QY 181 G1uLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuAspAsnArgHis 200
Db 553 GAACTCTGGGCTTCCAGCTCCGCGCTCCCAAACTGCGCCCTGCGCAAAAGGCGCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220
Db 613 AGTGTGCAACTGACCTGCTCCCTGGGCTAGAGATGCTGCGGTCCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrrGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CGGGCTGTGAGCTGCATCTGCACCTGGGGGCTGCAGTGCCTCGGGCTCGGAGCAACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGGAGATCCAGTGGTTACCTCAGCACCGCCTTTGCC 792

QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGGCCCGCGAGGCTGGCCGTGTGGCGCCCTTCTGGAG 852
QY 281 G1uGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 853 GAGGCGCGGAAACAAACAGTGCCTTAGACAACTTGCTGTCTGGGAAAGAAATCGCT 912
QY 301 G1uGluGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAGGCTCAGAGACTCAGTCCAGAGCTGACATATCTCCTCCCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProCysAlaGlnGlyVal 340
Db 973 TTCAGCCGCTACTTCCAAATATGAGGGGTCTGTACTACACCGCCCTGCGGGTGC 1032
QY 341 IleTrrThrValPheAsnGlnThrValMetLeuSerAlaAlaGlnLeuHisTrrLeuSer 360
Db 1033 ATCTGACTGTGTTTAACTCAGACGTGATGCTAAGACGCTCCACACCTCTCT 1092
QY 361 AspThrLeuTrrPglYProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGCTGTGTGACTCTCGGCTACACTGAACCTCCGAGGAGCGAGCCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1153 TTGAATGGGAGATGATGAGGCTCTCTCCCTGCTGAGTGGACAGCACTCTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCACTCAGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 G1yLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTCTCTGTCAACAGCTCGGCTCTCTGTCGAGATGAGAGGCGACAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAAACCAAGGGGGTGTGAGCTACCGCCAGCAGAGGTACCGAGACTGAGGCC 1389

RESULT 2
US-08-477-504A-1
Sequence 1, Application US/08477504A
Patent No. 5972353
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/477,504A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3D

TELECOMMUNICATION INFORMATION:

TELEPHONE: 415-435-2034
TELEFAX: 415-435-0272
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-477-504A-1

Alignment Scores:

Pred. No.:	7,09e-202	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	2	Gaps:	0

US-09-967-237A-2 (1-459) x US-08-477-504A-1 (1-1522)

QY 1 MetAlaProLeuCyPProSeProTTrpLeuProLeuLeuLeuProAlaProAlaProGly 20
DB 13 ATGGTCTCCCTGTGCTCCAGCCCTGCTCTCTCTGATCCCGCCCTGCTCAAGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 73 CTCACGTGCAACTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGlyAspAspProLeu 60
DB 133 CCGGAGGAGGAGGAGGATTCCTCTGGAGAGGCTCTTGGGAGAGATACCCACTG 192
QY 61 GlyGluGluAspLeuProSeGlnGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGGAGGAGGATCTGCTCCAGTCAAGAGATTCACCAAGAGAGAGATCCACCGGAGAG 252
QY 81 GluAspLeuProGlyGlyGluAspLeuProGlyGlyGluAspLeuProGluValAspPro 100
DB 253 GAGGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAGTTAAGCT 312
QY 101 LysSerGlnGluGluGlySerLeuLeuLeuLeuLeuProThrValGluAlaProGly 120
DB 313 AAATCAGAGAGAGAGGCTCCCTGAGATTAGAGATCTACCTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
DB 373 GATCTCTAAGAACCCCAATATATCCCAAGAGGACAAAGAGGAGATGACCAAGATCAT 432
QY 141 TrpArgTrpGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
DB 433 TGGGCTATGAGGAGGACCCGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCTGGGCT 492
QY 161 GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
DB 493 CAGTCCCGGAGGATATCCGCCCCCAGGCTCGCCCTCTGCCCCGCTGGGCTGGGCTGG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuLeuArgLeuArgAsnAlaHis 200
DB 553 GAATCTCTGGGCTTCAAGCTCCCGCCGCTCCCAAGATCGGCTCGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTrp 220
DB 613 AGTGTGCAATGACCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHisLeuHis 240
DB 673 CGGGCTGTGCAAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
QY 241 ValGluGlyHisArgPheProAlaGluLeuHisValHisLeuSerThrAlaPheAla 260

DB 733 GTGAGAGCCACCGCTTCCCTGCCGAGATTCACCGTGTTCACTCAGCAGCGCCCTTGGC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValAlaPheLeuGlu 280
DB 793 AGAGTTGACGAGGCTTGGGGGCGCCCGGAGGCTTGGCGCTTGGCTTGGAG 852
QY 281 GluGlyProGlnGluAsnSerAlaTrpGluGlnLeuLeuSerArgLeuGluGluLea 300
DB 853 GAGGCCCCGAGAGAAACAGTGCCTATGACAGATTGCTGTCTTCCCTTGAGAAATCCCT 912
QY 301 GluGluGlySerGluTrpGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
DB 913 GAGAGAGCTCAGAGACTCAGCTCCAGAGCTGACATATCTGCACTCCTCCCTCTGAC 972
QY 321 PheSerArgTrpPheGlnTrpGlyGlySerLeuThrTrpProProCysAlaGlnGlyVal 340
DB 973 TTCAGCCGCTTCTTCAATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGGGTTC 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisLeuLeuSer 360
DB 1033 ATCTGACTGTGTTTACACAGACAGTGAATGCTGAGTCTAAGAGCTTCAACCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
DB 1093 GACACCTGTGGGACCTGGTGACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB 1153 TTGAATGGGCGAGATTTGAGAGCTCTCTCTCTCTGAGTGAAGACAGATCTTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaPheLeuValAlaLeuValPhe 420
DB 1213 GCTGAGCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
DB 1273 GGCCTCTTTTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
QY 441 ArgGlyThrLysGlyGlyValSerTrpArgProAlaGluValAlaGluThrGlyVala 459
DB 1333 AGGGAGAACAAAGGGGGGTGAGCTACCGCCACAGAGGTAGCCGAGACTGGAGCC 1389

RESULT 3
US-08-486-756A-1
; Sequence 1, Application US/08486756A
; Patent No. 5981711
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 6 Mariposa Court
; CITY: Tiburon
; STATE: California
; COUNTRY: USA
; ZIP: 94920
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/486,756A
; FILING DATE: 07-JUN-1995
; CLASSIFICATION: 424
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3C
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-486-756A-1

Alignment Scores:
Pred. No.: 7.09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: Gaps: 0

US-09-967-237A-2 (1-459) x US-08-486-756A-1 (1-1522)

QY 1 MetAlaProLeuCySProSerProTPrLeuProLeuLeuIeProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTCGCTCCCGAGCCCTGCTGCTGTTGATCCCGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACCTGGACACTGCTGCTGTCACTGCTGCTTGTGATGCTTCCATCCCAAGGTTG 132
QY 41 ProArgMetGlnLysAspSerProLeuGlyGlySerSerGlyLysAspAspProLeu 60
Db 133 CCCCGAGTGCAGAGGATTCCTCCCTGGAGAGGCTCTTCGGGGAAGATGACCACTG 192
QY 61 GlyGlnLysAspLeuProSerGlnGlyLysAspSerProArgGlnGlyAspProGlyGlu 80
Db 193 GGGCGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGATCCACCGGAGAG 252
QY 81 GluAspLeuProGlyGlnGlyLysAspLeuProGlyGlnGlyLysAspLeuProGlyValLysPro 100
Db 253 GAGGATCTACCTGGAGAGAGATCTTACTCTGAGAGAGATCTTACTGAAATTAACTCT 312
QY 101 LysSerGlnGlnGlySerLeuLysLeuGlnLysLeuProThrValGlnAlaProGly 120
Db 313 AAATCAGAAAGAGGGCTCCCTCAAGTGAAGATCTTACTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGlnProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
Db 373 GATCTCAAGAACCCCGAATATATGCCACAGGACAAAGAGAGATGACCAAGTCAAT 432
QY 141 TrpArgTyrGlyLysAspProProTPrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGGGCTATGGAGCGACCCGCCCTGGGCCCGGGTGTCCCAAGCTGGCGGGCGGCTTC 492
QY 161 GlnSerProValAspLysArgProGlnLysAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCCACTCCGCCCTTTCGCCGCGGCTTCGCCGCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuAspProGlyLeuAspGlyLeuArgAsnAsnGlyHis 200
Db 553 GAACTCTGGGCTTCCAGCTCCGCCCTCCCAAACTGGCCCTGGCCGACAAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLysGlnMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTCAACTGACCTGCTCTGGGCTTGAAGATGCTGTGGTCCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTTrGlyValAlaGlyArgProGlySerGlnHisThr 240

Db 673 CGGGCTTCGAGCTGCATCTGCATCGGGGGGCTGCAGGCTCTCCGGGCTTCGAGCACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnLeuHisValValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCCTGCGAGATCACTGTTTCACTTCACTTCAAGCCCTTTGCC 792
QY 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280
Db 793 AGATTGACGAGGCTTGGGGCCCGGGAGGCTTGCCGTGTGGCCCGCTTCTTGAG 852
QY 281 GluGlyProGlnLysSerAlaTyrGlnGlnLeuLeuSerTrpLeuGlnGlnLeuAla 300
Db 853 GAGGGCCCGAAGAAAACATGCTGTATGACAGATGCTGTCTGTGGAAAGAAATGCT 912
QY 301 GluGlnGlySerGlnThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGCTCAGAGACTCAGTCCAGAGCTGGAATATCTGCACTCCGCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrProProCysAlaGlnGlyVal 340
Db 973 TTCAGCCGCTACTTCCATATGAGGGGCTCTGACTTACACCGCCCTGTGCCAGGGTGT 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaGlnLeuHisThrLeuSer 360
Db 1033 ATCTGACTGTGTTTAAACAGACAGTGAAGTGAAGTGAAGCTTCCACACCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyLysAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGCTGTGACTCTCGGCTACACTGAATCTCCGAGGAGAGCCCT 1152
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerProAlaGln 400
Db 1153 TTGAATGGCGAGATGATTGAGGCTCTTCCCTGCTGAGTGAACAGCTCTCCGGCT 1212
QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLysLeuValLeuValPhe 420
Db 1213 GCTGAGCAAGTCAAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHis 440
Db 1273 GGCCTCTTTTCTGTCACACAGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1332
QY 441 ArgGlyThrLysGlyValLysTyrArgProAlaGlnValAlaGlnThrGlyAla 459
Db 1333 AGGGAAACCAAGGGGGTGTGAGCTACCGCCAGAGAGTACCGAGACTGAGCC 1389

RESULT 4
US-08-485-862B-1
Sequence 1, Application US/08485862B
Patent No. 5989838
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MW Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (BPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,862B
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/477,504
FILING DATE: 07-JUN-1995
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021,JD
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-485-862B-1

Alignment Scores:
Pred. No.: 7,09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-967-237A-2 (1-459) x US-08-485-862B-1 (1-1522)

Qy 1 MetAlaProLeuCyProSerProThrLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTCGCCCCAGCCCTGGCTCTCTGTGATCCGGCCCCCTGCTCCAGGC 72
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 73 CTCACGTGCACTGCTGCT 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATGACAGAGATTCCTCCCTGGAGAGAGCTCTCTGGGGAAGATGACCCACTG 192
Qy 61 GlyGluGluAspLeuProSerGlyGluAspSerProArgGlyGluAspProGlyGlu 80
Db 193 GGCAGAGAGATCTGCCAGATGAGAGATTCACCCAGAGAGAGATCCACCGGAGAG 252
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValIlePro 100
Db 253 GAGGATCTACCTGAGAGAGAGATCTACCTGAGAGAGATCTACCTGAGATTAAGCTT 312
Qy 101 LysSerGlnGluGlnGlySerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 120
Db 313 AAATCAGAAAGAGAGGCTCCCTGAGATTAGAGATCTACCTGATTAGAGCTCTGGA 372
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspGlyGlyGlyAspAspGlnSerHis 140
Db 373 GATCTCAAGAAAGAGAGATTAAGTCCCAAGAGAGAGAGAGAGAGAGAGAGAGAGAT 432
Qy 141 TrpArgTyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGGCGCTATGAG 492
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaIlePheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGATGATTCGCCCAAGCTCGCGCTCTCTCTCTCTCTCTCTCTCTCTCTCT 552
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuAlaGluLeuArgAsnArgHis 200
Db 553 GAATCTCTGGGCTTCAGACTCCGCGCTCTCCCAAGACTGCGCTGCGCAAGAGAGAGAG 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220

Db 613 AGTGTCAACTGACCTGCTCTCTGGGCTAGAGATGCTCGGGTCCGGGCGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisIleThrGlyAlaAlaIleArgProGlySerGlnHisThr 240
Db 673 CGGCTCTGACGCTGCACTGCACTGGGGGGGCTGCAAGTCTCGGGCTCGAGACACT 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValHisIleLeuSerThrAlaPheAla 260
Db 733 GTGAGAGCCACCTTTCTCTGCGAGATCCAGCTGTTCACTTCACACCGCTTTGCC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaIlePheLeuGlu 280
Db 793 AGATTACAGAGGCTTGCGGGCGCCCGGAGAGCTGGCCGCTTGCGCTTCTGAGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerAlaGluGluIleAla 300
Db 853 GAGGCGCGGAG 912
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAGGCTCAGAGACTCAGCTCCAGAGCTGACATATCTGACTCTGCTCTGAC 972
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTGACCGCTACTTCCAAATAGAGGGGTCTCTGACTACACCGCTGCGCCAGGGTGC 1032
Qy 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaGlyGlnLeuHisIleThrLeuSer 360
Db 1033 ATCTGAGCTGTTTAAACAGACAGTATGCTGATGCTAGACAGCTCCACACCTCTCT 1092
Qy 361 AspThrLeuThrProGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGAGCTGTGACTCTCGGCTACAGCTGAATCTCCAGAGCAGAGCTT 1152
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGGAGAGATTTGAGAGCTCTCTCCCTGCTGAGTGCAGACAGATCTCGGAGCT 1212
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCTCTCTTTTGTGTGACCAAGGCTGCTCTCTTTGTGAGATGAGAGAGCAGACAGA 1332
Qy 441 ArgGlyThrIleGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGGAACCAAGGGGCTGTGAGCTACGCCAGACAGAGTACGAGACTGAGGCC 1389

RESULT 5
US-08-787-739-1
Sequence 1, Application US/08787739
Patent No. 6027887
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 96
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 369 Pine Street, Suite 610
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)

Sequence 1, Application us/08487077A
Patent No. 6069242
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/487,077A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3H
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-487-077A-1
Alignment Scores:
Pred. No.: 7,09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-967-237A-2 (1-459) x US-08-487-077A-1 (1-1522)
QY 1 MetAlaPProLeuCyPProSerProTThPLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGTCGCCAGCCCTGCTGCTCTGCTGATGCCCTGCTCCAGGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACCTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
QY 41 ProArgMetGlnGlnAspSerProLeuGlnGlnGlnSerSerGlnGlnAspAspProLeu 60
Db 133 CCCCGAGTGCAGAGAGATTCCCTTGGAGAGAGGCTCTTCTGGGGAAGATGACCCACTG 192
QY 61 GlnGlnGlnAspLeuProSerGlnGlnGlnAspSerProArgGlnGlnGlnAspProGlnGln 80
Db 193 GACGCGGAGATCTGCCCAAGTGAAGATTCACCCAGAGAGAGATTCACCCGAGAGAG 252
QY 81 GlnAspLeuProGlnGlnGlnGlnAspLeuProGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 100

Db 253 GAGGATCTACTGGAGAGAGATCTACTGAGAGAGAGATCTACTGAAATTAAAGCT 312
QY 101 LysSerGlnGlnGlnGlnGlnSerLeuLeuLeuLeuLeuLeuProTThValGlnAlaProGly 120
Db 313 AAATCAGAGAGAGAGGCTCCCTCAAGATTAAAGATCTACTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 140
Db 373 GATCTCAAGAACCCCAATTAATGCCCACAGGACAAAGAGGAGATGACCAAGTAT 432
QY 141 TrpArgTyrGlnGlnAspProProTThProArgValSerProAlaCyAlaGlnArgPhe 160
Db 433 TGGGCTATGAGAGGAGACCCGCTGAGCCCGGGGTGTCCTGAGCTGAGCGGCGGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCyAspProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCCAAGTCCCGCTTCCTCCGCGCTCCGCGCTCCGCGCTCCG 552
QY 181 GlnLeuLeuGlnPheGlnLeuProProLeuProGlnLeuAlaGlnArgAsnAsnGlnHis 200
Db 553 GAACTCTGGGCTTCCAGCTCCCGCTCCGCTCCCAAGACTGCGCTGCGCAATGCGCAC 612
QY 201 SerValGlnLeuThrLeuProProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 220
Db 613 AGTGCAACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisIleTyrGlnAlaAlaGlnArgProGlnGlnGlnGlnGln 240
Db 673 CGGGCTGCGACGTCATCTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 732
QY 241 ValGlnGlnHisIleArgPheProAlaGlnIleHisValAlaHisLeuSerThrAlaPheAla 260
Db 733 GTGAAGCCACCGCTTCCCTGCGAATCAAGTGTTCCTCCTCAGACCGCTTTCCTCC 792
QY 261 ArgValAspGlnAlaLeuGlnArgProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 280
Db 793 AGAGTTGACGAGGCTTGCGGCGCGCGCGGAGCGCTGCGGCTGCGGCTTCTTCTGAG 852
QY 281 GlnGlnGlnProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 300
Db 853 GAGGCGCCGGAAGAAACAGGCTTATGAGAGAGTGTCTGCTGCTGCTGGAAGAAATCCCT 912
QY 301 Gln 320
Db 913 GAGGAGGCTCAGAGACTCAGGCTCCAGAGCTGACATATCTGACTCTCCCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 340
Db 973 TTCAAGCGCTACTTCCAAATATGAGGGGTCTGACTACACCGCTGCGCCAGGATGTC 1032
QY 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisIleThrLeuSer 360
Db 1033 ATCTGACTGTGTTAACCAAGACAGTATGCTGAGTGTAAAGCAAGCTCCACACCTCTCT 1092
QY 361 AspThrLeuTyrPyrProGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 380
Db 1093 GACACCTGTGGGACCTGTGACTCTGCGCTTACAGCTGAACTTCCAGACGACGAGCT 1152
QY 381 LeuAsnGlnArgValIleGlnAlaSerPheProAlaGlnValAspSerSerProArgAla 400
Db 1153 TTGAATGGCGAGATTTGAAGGCTCTCTCTCTGAGAGTGAAGAGAGTCTCGGCT 1212
QY 401 AlaGlnProValGlnLeuAsnSerCyLeuAlaAlaGlnAspIleLeuAlaLeuValPhe 420
Db 1213 GCTAGCGACAGTCCAGTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlnLeuLeuPheAlaValIleThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTGTCTGTCACAGCGCTGCGCTTCTTGTGAGATGAGAGGACACACAGA 1332
QY 441 ArgGlnThrArgGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGlnGln 459
Db 1333 AGGGAACCAAGGGGGGTGAGCTACCGCCACAGAGTACCGGAGACTGAGGCC 1389

RESULT 7
US-08-485-863A-1
Sequence 1, Application US/08485863A
Patent No. 6093548
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: NM Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 6 Mariposa Court
CITY: Tiburon
STATE: California
COUNTRY: USA
ZIP: 94920
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,863A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/260,190
FILING DATE: 15-JUN-1994
ATTORNEY/AGENT INFORMATION:
NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3G
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-435-2034
TELEFAX: 415-435-0727
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-485-863A-1
Alignment Scores:
Pred. No.: 7,09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 3 Indels: 0
Gaps: 0
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QY 1 MetaAlaProLeuCySPSeProTPrLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTCGCCAGCCCTGAGCTCCTCTGTGATCCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuLeuLeuLeuLeuLeuLeuLeu 40
Db 73 CTCACCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATGAGAGGATTCCTCCCTTGAGAGAGGCTCTTGGGGAAGATGACCCACTG 192
QY 61 G1yGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
Db 193 GCGGAGAGGATCTGCCAGTGAAGAGATTCCACCCAGAGAGGATCCACCCGAGAG 252

QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyGlu 100
Db 253 GAGGATCTACCTGAGAGGAGGATCTACCTGAGAGAGGATCTACCTGAGAGGATCTACCTGAGAGGATCT 312
QY 101 LysSerGluGluGluGlySerLeuGlyGluGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGAGGCTCCCTGAAAGATTAGAGAGATCTACCTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGluGlyAspAspGlnSerHis 140
Db 373 GATCTTCAGAACCCCGAATATGCTCCACAGGAGCAAAAGAGGATGACCAATGATCAT 432
QY 141 TrpArgTyrGlyGlyAspProProTPrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGAGAGCGAGCCCGCTGAGCGGCTGCTCCACAGCTGCGGGGCGCTTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATATCCGCCAGCTCGCGCTTTCGCGGCTGCGGCTGCGGCTGCGGCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 553 GAACCTCTGGGCTTCCAGCTCCGCGGCTCCGGAACCTGCGCTGCGCAACATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGCACTGACCTGCTCTGCGGCTAGAGATGCTGCGGCTCCGCGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisSerProGlyAlaAlaGlyArgProGlySerGlyHis 240
Db 673 CCGGCTCTGAGTGAATGCACTGCGGGGCTGCGAGTGTCCGGGCTCGGAGCACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTTCCTGCGGAGATCCAGTGTTTCACTTCACTGACACCGCTTGGC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTGCGGTGTGGCCCTTCTTGAG 852
QY 281 GlnGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 853 GAGGGCCCGAATAAACAAGTGTCTATGAGCAATTGCTGTCTGTTGGAAGAAATCGCT 912
QY 301 GluGluGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGCTCAGAGACTCAGGTCCAGAGCTGGAATATCTGCACTCTCTGCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCAGCCGCTACTTCCAAATATGAGGGGTCTGACTACACCGCCCTGTGCGGGGTGTC 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisSerThrLeuSer 360
Db 1033 ATCTGACCTGTGTTTAAACAGACAGATGATGATGCTTAAGCAGCTCCACACCTCTCT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGGAAGCTGGTGACTCTGGGCTACAGCTGAACCTCGAGAGAGAGGCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1153 TTGAAATGGCGAGATGATTAAGGCTCTCTCCGCTGAGTGAACAGCATCTCCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTTCAGCTGAATTCCTGCGCTGCTGAGCACTCTTACCCCTGATTTT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GCGCTCTTTTCTGTCTACACAGCTCGCGTTCCTTGTGTCAATGAGAGGAGCAGCAGA 1332

|||||
Db 1273 GGCCTCTTTTGTGTCACCGAGCGTCCGTTCTTGACAGATGAGAGGACGACAGCA 1332
Qy 441 ArgGlyThrIysGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAAACCAAGGGGTGTGACTACCGCCACGACAGGTAGCCGAGACTGAGGCC 1389

RESULT 9
US-09-178-115-1
Sequence 1, Application US/09178115
Patent No. 6297041
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021.5A
CURRENT APPLICATION NUMBER: US/09/178,115
CURRENT FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 09/177,776
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 08/787,739
EARLIER FILING DATE: 1997-01-24
EARLIER APPLICATION NUMBER: 08/485,049
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/486,756
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/477,504
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/481,658
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,862
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,863
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/487,077
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/260,190
EARLIER FILING DATE: 1994-06-15
EARLIER APPLICATION NUMBER: 08/177,093
EARLIER FILING DATE: 1993-12-30
EARLIER APPLICATION NUMBER: 07/964,589
EARLIER FILING DATE: 1992-10-21
EARLIER APPLICATION NUMBER: PV-709-92
EARLIER FILING DATE: 1992-03-11
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1522
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(1389)
FEATURE:
NAME/KEY: mat_peptide
LOCATION: (124)..(1389)
US-09-178-115-1

Alignment Scores:
Pred. No.: 7.09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conserves: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 3 Gaps: 0

US-09-967-237a-2 (1-459) x US-09-178-115-1 (1-1522)

Qy 1 MetaIaProleuCySProSerProTyrProleuProleuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCTCCGACGCTGCTCCTCTGTGATCCCGGCGCTGCTCCAGGC 72

Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGCAACTGCTGCTGCTCACTGCTCTGTGATGCTCTTCATCCCGACAGGTTG 132
Qy 41 ProArgMetGlnIleuAspSerProLeuGlyGlySerSerGlyValuAspAspProLeu 60
Db 133 CCGCGATGAGAGAGATTCCTCCCTTGGAGAGGCTCTTCTGGGAAGTGACCACTG 192
Qy 61 GlyGlyIleuAspLeuProSerGluIleuAspSerProArgGluIleuAspProGlyIleu 80
Db 193 GCGAGAGAGATTCGCCACGATGAGAGATTCACCCAGAGAGAGATCCACCGGAGAG 252
Qy 81 GluAspLeuProGlyGlyIleuAspLeuProGlyGlyIleuAspLeuProGlyValIlePro 100
Db 253 GAGGATCTACCTGAGAGGAGATCTACCTGGAGAGAGATCTACCTGAGTTAAGCCT 312
Qy 101 LysSerGlnGluGlySerLeuIleuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGGCTCTCGAAAGTTAGAGATCTACCTGTTGAGGCTCTGGA 372
Qy 121 AspProGlnIleuProGlnAsnAsnAlaHisArgAspLysGluIleuAspGlnSerHis 140
Db 373 GATCTCAAGAACCCAGAAATATGCCACAGGAGCAAGAGGATGACAGATCAT 432
Qy 141 TyrArgTyrGlyIleuAspProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCGCTATGAGAGCACCCGCTGCGGCTGCTCCCACTGCGCGGCGCCCTTC 492
Qy 161 GlnSerProValAspIleArgProGlnIleuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGATTCGCCCCAGCTCGCCCTTGCCCGGCGCTGCGCCCTCG 552
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluIleuArgLeuArgAsnGlyHis 200
Db 553 GAATCTCGGCTTCAGCTCCCGCGCTCCGAGACTGGCGCTGGCAACATGGCCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyIleuGluMetAlaGluIleuProGlyArgGlyTyr 220
Db 613 AGTGTCAACTGACCTGCTCTGCGCTGAGATGAGATGCTGGTCCCGGCGGAGTAC 672
Qy 221 ArgAlaLeuGlnLeuHisIleuHisIleuTyrGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 673 CGGGCTCTGAGCTGATCTGCACCTGGGGGCTGCAGTGTCTCGGGCTCGAGACACT 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleuHisValHisIleuSerThrAlaPheAla 260
Db 733 GTGAAAGGCACCGTTTCCCTGCGAGATCCAGTGTCTCACTCGACACCGCTTGGC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyIleuAlaValIleuAlaPheLeuGlu 280
Db 793 AGAGTTGACGAGGCTTGGGCGCCCGGAGAGGCTGGCGGTGTGGCCGCTTTCGAG 852
Qy 281 GluGlyProGluIleuAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluIleuAla 300
Db 853 GAGGCCCCGAGAAACAGTGTCTATGACAGTTCCTGTGCTTGGAAAGAAACGCT 912
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGCTCAGGCTCCAGAGCTGACATATCTGCACTCTCGCCCTGAG 972
Qy 321 PheSerArgTyrPheGlnTyrGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCAGCGCTACTTCAATATGAGGGGTCTGTGACATCACCGCGCTGCCAGGGGTGC 1032
Qy 341 IleTyrThrValPheAsnGlnThrValMetLeuSerAlaIleGlnIleuHisIleuLeuSer 360
Db 1033 ATCTGACGTGTGTTAAACGACAGATGATGCTGAGTCAAGCACTCCACACCTCTCT 1092
Qy 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGACTGTGACTCTCGGCTACACTGAATCTCGAGCGAGCGAGCT 1152
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400

Db 1153 TTGAATGGCCAGTATTGAGCCCTCTCCCTGTGAGTGGACAGACAGTCTCGGGCT 1212
Qy 401 AAGAGProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTAGGCGAGTCCAGACTGAATTCCTGCTGCTGTGAGATCTTACCTGAGTCTTCTTCTT 1272
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTGTGCTGACACAGCGTCCGTTCTTGACAGATGAGAAGGACAGACAGA 1332
Qy 441 ArgGlyThrIysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAGACCAAGGGGCTGTAGCTACCCGCCAGAGAGTACCCGAGACTGGAGCC 1389

RESULT 10
US-09-177-776-1
Sequence 1, Application US/0917776A
Patent No. 6297051
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
FILE REFERENCE: D-0021.5A
CURRENT APPLICATION NUMBER: US/09/177,776A
EARLIER FILING DATE: 1998-10-23
EARLIER APPLICATION NUMBER: 08/787,739
EARLIER FILING DATE: 1997-01-24
EARLIER APPLICATION NUMBER: 08/485,049
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/486,756
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/477,504
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/481,658
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,862
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/485,863
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/487,077
EARLIER FILING DATE: 1995-06-07
EARLIER APPLICATION NUMBER: 08/260,190
EARLIER FILING DATE: 1994-06-15
EARLIER APPLICATION NUMBER: 08/177,093
EARLIER FILING DATE: 1993-12-30
EARLIER APPLICATION NUMBER: 07/964,589
EARLIER FILING DATE: 1992-10-21
EARLIER APPLICATION NUMBER: PV-709-92
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1
LENGTH: 1522
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (13) .. (1389)
FEATURE:
NAME/KEY: mat.peptide
LOCATION: (124) .. (1389)
US-09-177-776-1

Alignment Scores:

Pred. No.: 7.09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-967-237A-2 (1-459) x US-09-177-776-1 (1-1522)

Qy 1 MetAlaProLeuCybProSerProTribLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCCCTGCTCTCTGTGTATCCCGGCCCCCTGCCAGGC 72
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlyArgLeu 40
Db 73 CTCACGTGCACTGCTGTCTGTCACTGCTCTTGTGATGCTGTTCATCCCAAGAGTTG 132
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATGACAGAGATTCCTCCCTTGGAGAGAGCTCTTGAGGAAGATGACCACTG 192
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 193 GGCAGAGAGATCTGCCAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 252
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValIlePro 100
Db 253 GAGGATCTTACTGAGAGAGAGATCTTCTGAGAGAGAGATCTTACTGAAGTTAAGCT 312
Qy 101 LysSerGluGluGluGlySerLeuValLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAGAGAGAGGCTCCCTGAAGTTAAGAGATCTTACTGAGGCTCTGGA 372
Qy 121 AspProGluGluProGlnAsnAsnAlaHisArgAspIleGluGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCCAAGATTAAGCCACAGGAGCAAGAGGGATGACCAAGATCAT 432
Qy 141 TyrArgTyrGlyGlyAspProProTribProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGCGCTATGAGAGCGACCCGCCCTGGCCCCGGGTGTCCCAAGCTCCGCGGCGCTTC 492
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCCGGGTGATATCCGCCCCCACTCGCGCTTGTGCCCCGCGCTGCGCCCCCTG 552
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuAlaGlnAsnArgHis 200
Db 553 GAATCCTGGGCTTCCAGCTCCGCCCTCCCAAGATCGGCCGCCCAAGAGGCAC 612
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTCACTGACCTGCTCTGCGGTGAGATGCTGTGATCCCGGCGGAGATAC 672
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleProGlyAlaAlaGlyArgProGlySerGluHisThr 240
Db 673 CGGCTCTGACAGTGCATCTGCACTGGGGGCTGCAAGTGTGCTCGGCTCGAGACACT 732
Qy 241 ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla 260
Db 733 GTGAGAGCCACCGTTTCCCTGCGAGATCCACCTGTCTTCACTCAGACACCGCTTGGC 792
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValAlaLeuAlaPheLeuGlu 280
Db 793 AGAGTTACAGAGGCTTGGGGGCGCCCGGAGGCTGCGCTGTGGCTTCTTGAG 852
Qy 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
Db 853 GAGGCGCCGGAAGAAACAGTGCCTATGAGCAAGTGTGTCTGCTTGGAAAGAAATGCT 912
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGAGAGCTCAGAGACTCAGGTCACAGACTGCAATATCTGACCTCGCCCTTGAC 972
Qy 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTGAGCGCTACTTCCATATGAGGGTCTCTACATACACGCGCTGTGCGAGGGTGC 1032
Qy 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaIysGlnLeuHisIleThrLeuSer 360
Db 1033 ATCTGAGTGTGTTTAACTGAGAGATGATGCTGATAGCAGCTCCACACCTCTCT 1092

QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
DB 1093 GACACCTGTCGGGAGCCTGGGACTCTCGGTTACAGCTGAATCTCCAGAGCAGCACCCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
DB 1153 TTGATGTGGGAGATGATGAGGCTCTCTCTCTGAGATGAGACAGCTCTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaIleGlyAspIleLeuAlaLeuValPhe 420
DB 1213 GCTAGCGCATCCAGCTGAATCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValIleSerValAlaPheLeuValGlnMetArgArgIleIleArg 440
DB 1273 GGCCTCTTTTGTCTGTCACACGCGCTGCTCTGTCGATGATGAGAGCAGCAGACA 1332
QY 441 ArgGlyThrIleGlyValIleSerTyrArgProAlaGluValAlaGluThrGlyAla 459
DB 1333 AGGGGAACAAAGGGGTGTGAGCTACCGCCACAGAGTAAAGCCGAGACTGGAGCC 1389

RESULT 11

US-09-772-719B-1
Sequence 1, Application US/09772719B
Patent No. 6770438

GENERAL INFORMATION:

APPLICANT: Zavada, Jan
Pastorekova, Silvia
Pastorek, Jaromir
TITLE OF INVENTION: MN Gene and Protein
NUMBER OF SEQUENCES: 86
CORRESPONDENCE ADDRESS:
ADDRESSEE: Leona L. Lauder
STREET: 465 California Street, Suite 450
CITY: San Francisco
STATE: California
COUNTRY: USA
ZIP: 94104

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (BFO)

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/772,719B
FILING DATE: 30-Jan-2001

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/485,049

FILING DATE: 07-JUN-1995

ATTORNEY/AGENT INFORMATION:

NAME: Lauder, Leona L.
REGISTRATION NUMBER: 30,863
REFERENCE/DOCKET NUMBER: D-0021.3A-2
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-981-0332
TELEFAX: 415-981-0332

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
ANTI-SENSE: NO
SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-09-772-719B-1

Alignment Scores:

Pred. No.: 7,09e-202 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 4 Gaps: 0
US-09-967-237a-2 (1-459) x US-09-772-719B-1 (1-1522)

QY 1 MetAlaProLeuGlyAspSerProTyrPleuProLeuIleProAlaProGly 20
DB 13 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTTGTATCCCGGCCCTGACAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
DB 73 CTCACGTGCACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB 133 CCGCGATGAGAGAGGATTCCTCCCTGGAGAGAGGCTCTTCTGGGAAATGACCACTG 192
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
DB 193 GCGAGAGAGATCTGCCAGTGAAGAGATTCAACCAGAGAGAGATCCACCCGAGAG 252
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValLysPro 100
DB 253 GAGGATCTACCTGGAAGAGAGATCTACCTGAGAGAGAGATCTAGATTAGCCT 312
QY 101 LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
DB 313 AATTCAGAGAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTTAGAGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAlaHisArgAspGlyGluGlyAspAspGlnSerHis 140
DB 373 GATCCTCAAGAACCCCAATAATGCCCACAGAGCAAAAGAGGGATGACCAAGACTCAT 432
QY 141 TTPATGTYGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
DB 433 TGGCGCTATGAGAGGACCCGCTGCGCGGCTGCGCGGCTGCGCGGCTGCGCGGCTTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaIlePheCysProAlaLeuArgProLeu 180
DB 493 CATTCGCCGTGATATCCGCCGCCAGCTGCGCGCTTGTGCCGCCCTGCGGCCCTCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
DB 553 GAACCTCGGGCTTCAGCTCCGCGCCGCCAGAACTCGCTCGGCAACAATGCGCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
DB 613 AGTGTCAACTGACCTGCTCTGAGCTAGAGATGCTCTGGGTCCCGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaIleGlyArgProGlySerGlnHisThr 240
DB 673 CGGCTCTGAGCTGATCTGCACTGGGGGGCTGCAAGTCGTCGCGGCTCGAGCACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValHisLeuSerThrAlaPheAla 260
DB 733 GTGGAAGGCCACCGTTCCCTGCGAGATCCAGTGTTCACCTCGACACCGCTTTGGC 792
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValIleLeuAlaIlePheLeuGlu 280
DB 793 AGAGTTGAGAGAGCTTGGGGGCGCCCGGAGGCTTGGCTGTGGCCCTTCTCGAG 852
QY 281 GluGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluAla 300
DB 853 GAGGGCCGGAAGAAACAGTGTCTATGAGCACTGCTCTGCTTGGAGAAATCGCT 912
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerArg 320
DB 913 GAGGAAGGCTCAGAGACTCAGGCTCCAGAGACTGAGCATATCTGCACTCTGCGCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysValIleGlnVal 340
DB 973 TTCAGCGCTACTTCCATATGAGGGGTCTGTGACTACCGGCTGTGCGGAGGTGTC 1032

QY		401	AAGUpProValGlnLeuSenSerCysLeuAlaIaGIYAspLIleuAlaLeuValPhe	420
Db		1213	GCTGAACCACTCCAGCTGAATTCCTCCTGGCTGTGGACATCTTAGCCCTGGATT	1272
QY		421	GIyleuLeuPheAlaValThrSerValAlaPheLeuValGlmeArArgArgInHIsarg	440
Db		1273	GGCCTCCTTTTGGCTGTCAACCAGCGTCGGTTCCTTGTCAGATGAAAGGCACAGA	1332
QY		441	ARGGLYThrLYeGIyGIyValSerTYRArgProAlaGlUValAaGUthrGIyAla	459
Db		1333	ACGGGAACCAAAGGGGGTGTGAGCTACCGCCACAGAGAGGTACCGACACTGAGACC	1389
RESULT 13				
US-09-949-016-171				
Sequence 171, Application US/09949016				
Patent No. 6812339				
GENERAL INFORMATION:				
APPLICANT: VENTER, J. Craig et al.				
TITLE OF INVENTION: POLYMORPHISMS IN KNOWN GENES ASSOCIATED				
TITLE OF INVENTION: WITH HUMAN DISEASE, METHODS OF DETECTION AND USES THEREOF				
FILE REFERENCE: CL001307				
CURRENT FILING DATE: US/09/949,016				
PRIOR APPLICATION NUMBER: 60/241,755				
PRIOR FILING DATE: 2000-10-20				
PRIOR APPLICATION NUMBER: 60/237,768				
PRIOR FILING DATE: 2000-10-03				
PRIOR APPLICATION NUMBER: 60/231,498				
PRIOR FILING DATE: 2000-09-08				
NUMBER OF SEQ ID NOS: 207012				
SOFTWARE: FastSeq for Windows Version 4.0				
SEQ ID NO: 171				
LENGTH: 1552				
TYPE: DNA				
ORGANISM: Human				
US-09-949-016-171				
Alignment Scores:				
Pred. No.:	7.3e-202	Length:	1552	
Score:	2424.00	Matches:	459	
Percent Similarity:	100.00%	Conservative:	0	
Best Local Similarity:	100.00%	Mismatches:	0	
Query Match:	100.00%	Indels:	0	
DB:	4	Gaps:	0	
US-09-967-237A-2 (1-459) x US-09-949-016-171 (1-1552)				
QY		1	MetaLaProLeuCysProSeerProTriPLeuProLeuLeuIleProAlaProAlaProGIy	20
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QY		21	LeuthrValGlnLeuLeuLeuSerLeuLeuLeuLeuMeCProValHisProGlnAArgLeu	40
Db		103	CTCACCTGTGCAACTGTGTCTGTACACGTGCTTCTATGTCTGTCCATCCCCAGAGTTG	162
QY		41	ProArgMetGlnGluAspSerProLeuGlyGIyGlySerSerGIyGluAspAspProLeu	60
Db		163	CCCCCGATCAGAGAGATTCCCCTTTGGAGAGAGGCTCTTTGGGAAAGATGCCACTG	222
QY		61	GIyGlnGluAspLeuProSeerGIyGluAspSerProArgGIyGluAspProProGIyGlu	80
Db		223	GGCGAGAGAGATCTGGCCCACTGTAAGAGATTCAACCCAGAGAGAGAGATCCACCGGAG	282
QY		81	GIUAepleuPProGIyGIyGluAspLeuPProGIyGIyGluAspLeuPProGIyValIysPro	100
Db		283	GAGGATCTAACCTCGGAAGAGATTCACCTCGGAGAGAGAGATTCACCTGAAGTTAGCCT	342
QY		101	IYssSerGIyGlnGluGIySerLeuIysLeuGluAspLeuProThrValGIuaIaPProGIy	120
Db		343	AAATCAGAAAGAGGGCTCCCTCGAAGTTAAGAGATCTACTACTGTGAGGCTCTCGGA	402
QY		121	AsPProGlnGluPProGlnAnAnAlaHisArgAspLyseGIyGluIYAspAspGlnSerHis	140

Dd	403	GATCCTCAGAAACCCAGATTAATGCCACAGGACAAAGAGGGATGACCAAGTCTAT	462
Qy	141	TPPAATGYTGYGlyAspProProTTPProArGVaSerProAlaCYsAlaGlyArGVhe	160
Dd	463	TGGGGCTATTGGAAGGGAGACCGCCCTGGGCCGGGGTGTCCCAAGCTGGGGCGGCTTC	522
Qy	161	GlInserProVaLaApplLeArGVProGlnLeuAlaAlaPheCYsProAlaLeuArGVProLeu	180
Dd	523	CAGTCCCGGGAGATATCCGGCCCCAGCTCCGCCCTTCTGCCCCGGCCCTGGCCCCCTG	582
Qy	181	GlInLeuLeuGlyPheGlnLeuProProLeuProGlnLeuAlaGlyLeuArGVAsnAsnGlyHis	200
Dd	583	GAACTCCCTGGGCTTCCAGCTCCGGCGCTCCCAAGATCGCCCTGGCGCAATAGGCCAC	642
Qy	201	SeArVaGlnLeuThrLeuProProGlyYLeuGlnMeAlaLeuGlyProGlyArGVAluTr	220
Dd	643	AGTGTGCAACTGACCCCTGCTCCCTGGGGTACATGGCTCTGGGTCCCGGGCGGGAATAC	702
Qy	221	ArGVAlaLeuGlnLeuHisLeuHisLeuTTPGlyValAlaAlaGlyArGVProGlySerGlnHisThr	240
Dd	703	CGGGCTCTGCAGCTGCATCTGCACCTGGGGGGCTCAGGTCCTCCGGGCTCCGACACACT	762
Qy	241	ValGlnGlyHisArGVProProAlaGlnLeuHisValValHisLeuSerThrAlaPheAla	260
Dd	763	GTGGAAGGCCACCGTTTCTCCCTGGCCGAATCCACGGTGTACCTCCAGACCGGCTTGGCC	822
Qy	261	ArGVAlaAspGlnAlaLeuGlyArGVProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln	280
Dd	823	AGAGTGAACGAGGCTTGGGGCGGCCGGAGAGCCTGGCGCTTGGCGGCTTCTGGAG	882
Qy	281	GlnGlyProGlnGlnLeuAsnSerAlaTyrGlnGlnLeuLeuSerArGVLeuGlnIleAla	300
Dd	883	GAGGGCCCGGAAGAAACAGTGCCTATGACGATGGCTGTCTCCCTGGAAAGAAATGCT	942
Qy	301	GlnGlnGlnGlySerGlnIleThrGlnValProGlyLeuAsnIleSerAlaLeuLeuProSerAsp	320
Dd	943	GAGGAAGGCTCAGAGACTCAGGCTCCAGAGATGACATGTGACTCTCGCCCTCGAC	1002
Qy	321	PheSerArGVTrPheGlnTyrGlnGlySerLeuThrThrProProCYsAlaGlnGlyVal	340
Dd	1003	TTCAGCCGCTACTTCCAAATAGAGGGGCTCTGACTACACGCCCTGTGGCCAGGGTCTC	1062
Qy	341	IleTTPThrValPheAsnGlnThrValMetLeuSerAlaIuGlyGlnLeuHisThrLeuSer	360
Dd	1063	ATCTGAGACTGTGTTAACCAAGACAGTAGCTGTAGTGTAGCAGCTCCACACCTCTCT	1122
Qy	361	AspThrIleuTTPGlyProGlyAspSerArGVLeuGlnLeuAsnPheAlaGlyAlaThrGlnPro	380
Dd	1123	GACACCCCTGGGGAGCCTGTGACTCTCGCTACAGCTGAACCTTCCGAGCAGACAGCT	1182
Qy	381	LeuAsnGlyArGVAlaIleGlnAlaSerPheProAlaGlyValaAspSerProArGVAla	400
Dd	1183	TTGAAATGGCCAGATGATTGAGGCTCTCTTCCCTGCTGAGATGGACAGACAGTCTCGGGCT	1242
Qy	401	AlaGlnProValaGlnLeuAsnSerCYsLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
Dd	1243	GCTGAGCAGATCCAGCTGAATTCTCTGCTGCTGTGATGACATCTAGCCCTGTGTTTT	1302
Qy	421	GlyLeuLeuPheAlaValaThrSerValAlaPheLeuValaGlnMetArGVArGVGlnHisArGV	440
Dd	1303	GGCTCTCTTTTGTGTGCACCAAGGTGGCGTCTCTTGTGCAGATGAAGGACACACAGA	1362
Qy	441	ArgGlyThrIuGlyGlyValSerTyrArGVProAlaGlnValaAlaGlnIleThrGlyVala	459
Dd	1363	AGGGGAACCAAGGGGGTGTAGCTACCGCCACAGATGTAGCCGAGACTGGAGCC	1419


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; NAME/KEY: misc_feature
; LOCATION: (1) ..(5052)
US-08-260-190-23

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Alignment Scores:

Pred. No.:	1.9e-184	Length:	5052
Score:	223.00	Matches:	451
Percent Similarity:	98.05	Conservative:	2
Best Local Similarity:	97.624	Mismatches:	6
Query Match:	92.128	Indels:	8
DB:	4	Gaps:	0

US-09-967-237A-2 (1-459) X US-08-260-190-23 (1-5052)

QY	MeVlaIaProLeuCYpProSerProTrieuProLeuLeuIleProAlaProAlaProGly	20
Db	ATGGCTCCCTGTGGCCAGCCCTTGACTCCCTCTGTGATCCCGGCCCTGTCTCAAGC	3604
QY	LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu	40
Db	CTCACTGTGCAACTGTCTGTCTCACTGTGCTTCTGATGCTGTGTCATCCCAAGAGTTGG	3664
QY	ProArgMetGlnGlnuAspSerProLeuGlyGlyGlySerSerGlyGlyuAspAspProLeu	60
Db	CCCCGGATGCGAGAGGATTC-CCCCCTTGAGAGAGGCTCTTCTGGAGGAAGATGCCACTG	3723
QY	GlyGlnuAspLeuProSerGlyGlyuAspSerProArgGlnGluAspProProGlyGlyu	80
Db	3724 GGCAGAGAGGATCTGCCCACTGGAAGAGGATTCACCCAGAGAGAGGATCCACCGGAGAG	3783
QY	GluuAspLeuProGlyGlyGlnuAspLeuProGlyGlyGlyuAspLeuProGluValLeu-Pr	100
Db	3784 GAGATATCTACCTGGAGAGAGGATCTCACTGGAGAGGAGATCTCACTGAAGTTAAATGCC	3843
QY	OLySerSerGlnGlnGlnGlySerLeuValSerLeuGluuAspLeuProThrValGluAlaProGly	120
Db	3844 TAAATCGAAGAAAGAGGCTCCCTCGAAGTTAGAGATCTTACTTCTGTGAGGCTCTCGG	3903
QY	YAspProGlnGlnuProGlnAsnAsnAlaHisArgAspIysGlnGlyAspAspGlnSerHis	140
Db	3904 AGATCCCTCAGAAACCCCGAATTAATGCCACAGGACCAAAAGAGGATGACAGAGATCA	3963
QY	STPrArgTyrGlyGlyAspProProTPrProArgValSerProAlaCysAlaGlyArgAspH	160
Db	3964 TTGGCGCTATGAGAGCGACCCGCC-TGGCCCCGGGTGTCCCAAGCTGGCGGGCGGCTT	4022
QY	eGlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLe	180
Db	4023 CCAAGTCCCCGGGTGATATCCGCCCCAGCTGGCGGCTTGTGCCCGGCGCTGGCGCCCT	4082
QY	uGlnuLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnArgGlyHis	200
Db	4083 GGAATCCTCGGGCTTCCAGCTCCGGCGCTCCAGAAATGGCGCTGCA-GACAAATGGCGCA	4141
QY	SerValGlnLeuThrLeuProProGlyLeuGluMetValaLeuGlyProGlyArgGlyTyr	220
Db	4142 CAGGTGCAATGACCTCGCTCTCGGGCTAGAGATGCTTGGGTCCCGGGCGGGAGTA	4201
QY	ArgAlaLeuGlnLeuHisLeuHisSTPrGlyValaAlaGlyValArgProGlySerGlnHisSTH	240
Db	4202 CCGGCT-CTGCAGCTGCATCTGCACCTGGGGGGCTGCAAGTGTGTCGGGCTCGAGACAC	4260
QY	rValGlnGlyHisArgPheProAlaGlnIleHisValValaHisLeuSerThrAlaPheAla	260
Db	4261 TGTGAAAGGCCACCGTTTCCCTGCCGAGATCAAGTGTCTCACTCCACACCGGCTTTGC	4320
QY	ArgValAspGlyuAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGly	280
Db	4321 CAGAGTTGACAGAGCGCTTGGGGCGCCGGGAGGCGCTGGCGTGTGGC-GCCTTCTTGGA	4379
QY	uGlnuGlyProGlnuAsnSer-AlaTyrGlnGlnLeuLeuSerArgLeuGlnGluIleAla	300
Db	4380 GGAGGGCCCGGAAATAACATGTCTCTATGAGCAAGTGTCTCTCGCTTGGAAATAATCG	4439

QY	360	aaagluGluGlySerGlnThrClnAlaProGlyLeuAspLleSerAlaLeuLeuProSerA	320
Db	4440	CTGAGGAAGGCTCAGAGACTAGAGCTCCAGACTGGACATATCTGCACTCTGCCCCCTG	4499
QY	320	spPheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyV	340
Db	4500	ACTTCAGCGCGTACTCTCCATATATGAGGGGCTCTGACTACACCGCCCTGTGCCAGGGTG	4558
QY	340	allIleTPrThValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisThrLeuS	360
Db	4560	TCATCTGACCTGTGTTTAAACGACGAGGATGCTGAGCTTACACAGCTCCACACCCCT	4619
QY	360	erAspThrLeuTirPglYProGlyAspSerArgLeuGlnLeuAspPheArgAlaThrGlnP	380
Db	4620	CTGACACCCCTGTGGGAGCTGCTGACTCTGGCTACAGCTGAACCTCCGACGACGACG	4679
QY	380	roLeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgA	400
Db	4680	CTTTGAATGGGCGAGTGATGATGAGCCCTCTCTCCCTGCTGGAGTGAGACGACGATCCTCGGG	4739
QY	400	laaIaGlnProValGlnLeuAsnSerCysLeuAlaIaAGlyAspLleLeuAlaLeuValP	420
Db	4740	CTGCTGAGCCACGCTCAGCTGAATTCCTGCTCGGCTGCTGGAGACATCTTACCCCTGGTTT	4799
QY	420	heGlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisA	440
Db	4800	TTGGGCTCTTTTTGCTGTGCACGACGCGCGCTTCTTGTCAGATGAGAAGGCGACACA	4859
QY	440	rgaArgGlyThrLysGlyValSer-TyrArgProAlaGluValAlaGlnThrGlyAlaA	459
Db	4860	GAAAGGGACCAAAAGGGGTGTGAGCGTACCGCCACGACGAGGTGACCGAATCTGAGACC	4919

Search completed: August 20, 2005, 01:29:39
Job time : 275 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame_plus_p2n model

Run on: August 19, 2005, 21:25:55 ; Search time 4549 Seconds
(without alignments)
3840.734 Million cell updates/sec

Title: US-09-967-237a-2

Perfect score: 2424
Sequence: 1 MAPLCBPMLPLIPAPAPG.....RRGKGGVSRPAVAETGA 459

Scoring table:

BLOSUM62
Xgapop 10.0 , Xgapext 0.5
Ygapop 10.0 , Ygapext 0.5
Fgapop 6.0 , Fgapext 7.0
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Command line parameters:

-MODE=frame+g2n.model -DEV=xlh
-Q=/cgn2_1/USPTO.spool/US09967237/runat_18082005_102618_117/app_query.fasta_1.647
-DB=EST -QMT=fastap -SUPFI=p2n.rst -MINMATCH=0.1 -LOOFCU=0 -LOOPEXT=0
-UNITS=bits -START=1 -END=1 -MATRIX=biosum62 -TRANS=human40.cdi -LIST=45
-DOCALLIGN=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL
-OUTFMT=pic -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000
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-NO_MMAP -LARGEQUERY -NEG_SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -Fgapop=6
-Fgapext=7 -Ygapop=10 -Ygapext=0.5 -Delop=6 -Delext=7

Database :

EST:
1: gb_est1.*
2: gb_est2.*
3: gb_hic.*
4: gb_est3.*
5: gb_est4.*
6: gb_est5.*
7: gb_est6.*
8: gb_gss1.*
9: gb_gss2.*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length DB	ID	Description
1	2420	99.8	1469	3	CR616345 full-leng
2	2420	99.8	1523	3	CR620502 full-leng
3	2420	99.8	1541	3	CR597234 full-leng
4	2361.5	97.4	1492	3	CR590646 full-leng
5	1790	73.8	1084	1	AL542336
6	1567	64.6	1070	1	AL554705
7	1556.5	64.2	1009	1	AL558378
8	1501.5	61.9	1017	5	AL558378
9	1472	60.7	916	5	BX423970

10	1452.5	59.9	971	7	COS79387
11	1401	57.8	927	1	AL555184
12	1332	55.0	1071	1	AL554665
13	1304.5	53.8	874	4	BG386425
14	1211	50.0	836	5	BX383092
15	1130	46.6	740	7	CR971835
16	1121	46.2	1017	1	AL580216
17	1115	46.0	994	1	AL577748
18	1114	46.0	668	4	BG824243
19	1113	45.9	818	2	BE548062
20	1092	45.0	782	7	CR696500
21	1090	45.0	761	5	BX423969
22	1075	44.3	722	7	CR978804
23	1064.5	43.9	746	4	BI223232
24	1060.5	43.8	806	2	BE344769
25	1041	42.9	589	4	BM790508
26	1041	42.9	813	7	CO734371
27	1002.5	41.4	736	2	BE543633
28	989	40.8	830	7	CR849799
29	986.5	40.7	945	7	CF579370
30	965	39.8	715	7	CR63805
31	945.5	39.0	649	6	BY735107
32	940	38.8	717	2	AW701559
33	932	38.4	709	7	CR65416
34	919.5	37.9	733	4	BG819731
35	910	37.5	682	1	AI831707
36	904	37.3	689	1	CA425935
37	886	36.6	551	6	CA406362
38	886	36.6	691	5	BU620600
39	879	36.3	502	7	CV029038
40	877.5	36.2	795	2	AM083555
41	862	35.6	668	7	CR624271
42	851	35.1	669	1	AI925646
43	847	34.9	489	1	AI791726
44	836	34.5	658	1	AI769526
45	830.5	34.3	582	4	BI534892

ALIGNMENTS

RESULT 1
CR616345
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS
SOURCE
ORGANISM
REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
COMMENT
FEATURES
source

CR616345 1469 bp mRNA linear HTC 21-JUL-2004
Full-length cDNA clone CSOD4003YB12 of Neuroblastoma of Homo sapiens (human).
CR616345
CR616345.1 GI:50497152
HTC; CNSLT CDNA.
Homo sapiens (human)
Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 1469)
Li, W.B., Gruber, C., Jessee, J., and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL: http://fulllength.invitrogen.com/Invitrogen Corporation 1600 Faraday Avenue
2 (bases 1 to 1469)
Genoscope.
Direct Submission
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage : BP 191 91006 Evry cedex - FRANCE (E-mail: seqref@genoscope.cns.fr - web: www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen.
Location/Qualifiers
1. 1469
/organism="Homo sapiens"

ORIGIN

/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DA003YB12"
/tissue_type="Neuroblastoma"
/plasmid="pCMVSPORT_6"

Alignment Scores:

Pred. No.: 2,44e-185 Length: 1469
Score: 2420.00 Matches: 458
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.83% Indels: 0
DB: 3 Gaps: 0

US-09-967-237A-2 (1-459) X CR616345 (1-1469)

QY 1 MetAlaProLeuCyPProSerProTTPLeuProLeuLeu1LeProAlaProGly 20
Db 5 ATGGCTCCCTGGCCCCAGCCCCCTGCTCTGTGAATCCCGGCCCTGCTCCAGGC 64
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 65 CTCACTGTGAACTGCTGCTGTCACTGCTTCTGTGCTGTCTCCATCCCGAGAGTTG 124
QY 41 ProArgKerGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 125 CCCCGAGTGCAGAGAGATCCCTCCCTGGAGAGAGCTCTTGCGGAAATGACCCACTG 184
QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 185 GGGGAGAGAGATCTGCCAGATGAAGAGATTCACCGAGAGAGAGATCCACCCGAGAG 244
QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValLysPro 100
Db 245 GAGGATTTACTGTGAGAGAGAGATCTACTGAGAGAGAGATCTACTGTTGAGAGCTCTGGA 304
QY 101 LysSerGlnGluGluGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 305 AAATCAAGAAAGAGAGGCTCCCTGAAGTTAGAGATCTACTGTTGAGAGCTCTGGA 364
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis 140
Db 365 GATCTCTCAAGAAACCCGAAATTAAGCCACAGAGGACAAAGAGGATGACAGAGTCAT 424
QY 141 TrpArgTyrglyGlyAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe 160
Db 425 TGGCGCTATGAGAGCGACCCGCCCTGGCCCCGGGTGTCCCGAGCTTCGGGGCGCTTC 484
QY 161 GlnSerProValAspLeuArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 485 CAGTCCCGGGTGGATATCCGCCCACTGCGCGCTTGCCTCCGGCGCTGCGCGCTCG 544
QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuAsnAsnGlyHis 200
Db 545 GAACCTCTGGAGCTTCAGCTCCGCCCTCCCAACTGGCGCTGCGCAACAAATGGGCAC 604
QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
Db 605 AGTGTGAACTGACCTGCTCTCGGGCTAGAGATGCTCTGGGTTCCTCCGGCGGAGATAC 664
QY 221 ArgAlaLeuGlnLeuHisLeuHisIleTyrglyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 665 CGGGCTCTGAGAGCTGCACTGCACTGGGGGCTGCAAGTGTGCTCGGGCTCGGAGCACT 724
QY 241 ValGluGluHisArgPheProAlaGluLeuHisValValHisLeuSerThrAlaPheAla 260
Db 725 GTGGAAAGCCACCTTTTCCCTGCGAGATCCACTGTGTTCACCTCCAGACCCGCTTTGGC 784
QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 785 AGAGTTACAGAGGCTTGGGGCGCCCGGAGAGCTGCGGTGTGGCCGCTTTCTTGAG 844

QY 281 GluGlyProGluGluAsnSerAlaTyrgluGlnLeuLeuSerArgLeuGluGluAla 300
Db 845 GAGGCGCCGGAAGAAACAGTGTCTATGAGCACTGCTGCTGTGAAAGAAATGCT 904
QY 301 GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 905 GAGGAAGCTCAAGACTCAGGTCCAGAGCTGAGCATATCTACCTCCGCTCTGAC 964
QY 321 PheSerArgTyrgPheGlnTyrglyGlySerLeuThrThrProCysAlaGlnGlyVal 340
Db 965 TTCAAGCCGCTACTTCCATATGAGGGGTCTCTACATACACCGCCCTGTGCCAGGGTGC 1024
QY 341 IleTyrgThrValPheAsnGlnThrValMetLeuSerAlaIsglnLeuHisIleThrLeuSer 360
Db 1025 ATCTGAGTGTGTTAACCAAGACATGATGCTGATGAGCAGGTCCACACCTCTCT 1084
QY 361 AspThrLeuThrGlyProGlyAspSerArgLeuGluLeuAsnPheArgAlaThrGlnPro 380
Db 1085 GACACCTGTGGAGACTGTGACTCTCGCTACAGCTGAATTCGAGGAGAGAGAGCT 1144
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1145 TTGAATGGCGGAGATGATGAGGCTCTCTTCCCTGCTGAGTGGACAGCACTCCGGCT 1204
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1205 GCTGAGCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1264
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1265 GGCCTCTTTTCTGTGACACAGCTGCTGCTTCTTGTGCAATGAGAAAGGACACAGA 1324
QY 441 ArgGlyThrTyrglyGlyValSerTyrgProAlaGluValAlaGluThrGlyAla 459
Db 1325 AGGGAACCAAGAGGGGTGTGACTACCGCCAGCAGAGATTACCGAGATGGAGCC 1381

RESULT 2
CR620502
LOCUS
DEFINITION
Full-length cDNA clone CS0DK007YK10 of HeLa cells Cot 25-normalized
of Homo sapiens (human).

ACCESSION
CR620502.1 GI:50501309
VERSION
CR620502.1
KEYWORDS
HTC; CNSLT_cDNA.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.

REFERENCE
AUTHORS
TITLE
JOURNAL
REMARK
1 (bases 1 to 1523)
La,W.B., Gruber,C., Tessee,U. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished
Contact : Feng Liang Email : fliang@lifetech.com URL :
http://fulllength.invitrogen.com/ Invitrogen Corporation 1600
Barclay Avenue
2 (bases 1 to 1523)
Genoscope.
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
Submitted (20-JUL-2004) Genoscope - Centre National de Sequencage :
BP 191 91006 EVRY cedex - FRANCE (E-mail : seqref@genoscope.cns.fr
- Web : www.genoscope.cns.fr)
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
source
Location/Qualifiers
1..1523
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DK007YK10"
/tissue_type="HeLa cells Cot 25-normalized"

ORIGIN /plasmid="pCMVSPORT_6"

Alignment Scores:

Prod. No.: 2,566-185 Length: 1523
Score: 2420.00 Matches: 458
Percent Similarity: 100.00% Conservative: 1
Best Local Similarity: 99.78% Mismatches: 0
Query Match: 99.83% Indels: 0
DB: 3 Gaps: 0

US-09-967-237a-2 (1-459) x CR620502 (1-1523)

Qy 1 MetAlaProLeuCyProSerProTrPleuProLeuLeuIleProAlaProAlaProGly 20
Db 32 ATGGCTCCCTGTGCCCCAGCCCCCTGGCTCCCTGTTGATCCCGCCCCCTCTCCAGGC 91
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 92 CTCACGTGCAACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 151
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGluAspAspProLeu 60
Db 152 CCCCAGATGCAAGAGATTCCTCCCTGGAGAGAGCTCTTCTGGGAGATGACCCACCTG 211
Qy 61 GllGllGluAspLeuProSerGllGluAspSerProArgGllGluAspProGlyGlu 80
Db 212 GCGGAGAGATCTCCCAAGTGAAGATTCACCAAGAGAGAGATTCACCCGAGAG 271
Qy 81 GllAspLeuProGlyGlyGluAspLeuProGlyGlyGluAspLeuProGlyValIlyPro 100
Db 272 GAGGATCTACCTGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAGATTAAGCT 331
Qy 101 LysSerGllGluGlyGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 332 AAATCAGAGAGAGAGAGCTCCCTGAGATTAAGATTAACCTGAGAGCTCTCGA 391
Qy 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGllGlyAspAspGlnSerHis 140
Db 392 GATCTCTAAGAACCCCAAGATTAATGCCACAGAGAGACAAAGAGAGATGACCAAGTCA 451
Qy 141 TrpArgTrpGlyGlyAspProProTrPProArgValSerProAlaCysAlaGlyArgPhe 160
Db 452 TGGGCTTANAGAGGAGACCCGCTGGCCGCGGAGTCCCAAGCCTGGCGGCGGCTTC 511
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 512 CAGTCCCGGAGATATCCGCCCAAGCTCCGCTCTGCTGCGCGGCTGGCGCCCTG 571
Qy 181 GllLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLysArgAsnAsnGlyHis 200
Db 572 GAACTCTGGGCTTCAGCTCCGCGCTCCCAAGATGCGCTCGGACAAATGAGCCAC 631
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlnTr 220
Db 632 AGTGGAACAGAACCTGCTCTCTGGGCTAGAGATGGCTCGGCTCCGCGGAGAGTAC 691
Qy 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 692 CCGGCTCTGACGCTCATCTGCACTGGGAGGCTGCAAGCTCGCCGCGCTCGAGACACT 751
Qy 241 ValGlnGlyHisArgPheProAlaGlnIleHisValValHisLeuSerThrAlaPheAla 260
Db 752 GTGAAAGGCACCGCTTCCTCCGCAAGATCAAGTGTACCTCAAGACCGCTTGGC 811
Qy 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln 280
Db 812 AGAGTTGACAGAGCTTGGGAGGCGCGGAGAGCTGGCGTGTGGCCGCTTCTGGAG 871
Qy 281 GllGlyTrpGlnGluAsnSerAlaTrpGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
Db 872 GAGGCGCCGGAAGAAACAGTGCCTATGAGCAGTGTGCTGTCTGGAAATAATCGCT 931

Qy 301 GllGlnGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 932 GAGGAAGGCTCAGAGACTCAGGTCCCAAGACTGAGCATATCTGCACTCTGCTCTGAC 991
Qy 321 PheSerArgTrpPheGlnTrpGlnGlySerLeuThrTrpProProCysAlaGlnGlyVal 340
Db 992 TTCAGCCCTCACTTCCCAATATGAGGGGCTCTGATACACCGCCCTGGGCCAGAGTGC 1051
Qy 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisThrLeuSer 360
Db 1052 ATCTGAGCTGTGTAAACCAAGCACTGATGCTGATGCTGATGCTGATGCTGATGCTG 1111
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1112 GACACCTCTGGGAGACCTGGTGACTCTGGGCTGACAGCTGAACCTTCGAGCGACGAGCT 1171
Qy 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1172 TTGAATGGGCGAGTATTAAGAGCTCTCTCCCTGCTGAGAGTGAACAGAGTCTCGGCT 1231
Qy 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1232 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1291
Qy 421 GllLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1292 GGCCTCTTTTGTGCTGATCAGAGCTCCGCTTCTGTCAGATGAGAGAGAGACAGCA 1351
Qy 441 ArgGlyThrLysGlyGlyValSerTrpArgProAlaGluValAlaGlnThrGlyAla 459
Db 1352 AGGGAGAACAAAGGGGGTGTGAGTACCGCCAGAGAGTACCGAGACTGAGACC 1408
RESULT 3
CRS97234 1541 bp mRNA linear HTC 21-JUL-2004
LOCUS full-length cDNA clone CSOD1085YF18 of Placenta Cot 25-normalized
DEFINITION of Homo sapiens (human).
ACCESSION CRS97234
VERSION CRS97234.1 GI:50478041
KEYWORDS HTC; CNSLT_CDNA.
SOURCE
ORGANISM Homo sapiens (human)
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1 (bases 1 to 1541)
Li, W.B., Gruber, C., Jeesee, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished
Contact: Feng Liang Email: fliang@lifetech.com URL:
http://fulllength.invitrogen.com/Invitrogen Corporation 1600
Paradise Avenue
2 (bases 1 to 1541)
REFERENCE
AUTHORS
TITLE
JOURNAL
COMMENT
1st strand cDNA was primed with a NotI-oligo(dt) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
was normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
FEATURES
location/Qualifiers
1..1541
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSOD1085YF18"
/tissue_type="Placenta Cot 25-normalized"
/plasmid="pCMVSPORT_6"

Alignment Scores:

Best Local Similarity: 97.82% Mismatches: 0
 Query Match: 97.42% Indels: 9
 DB: 3 Gaps: 1

US-09-967-237a-2 (1-459) x CR590646 (1-1492)

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QY 1 MetAlaPLeuCyAProSerProTribLeuProLeuLeuLeuProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGCCCCAGCCCTGGCTCCCTCTTGATCCCGCCCTGCTCAAGC 102
QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACTGCAACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 162
QY 41 ProArgMetGlnGlnuAspSerProLeuGlyGlySerSerGlyGlnuAspProLeu 60
Db 163 CCCCAGAGAGAGAGAGATTCCTCCCTGGAGAGAGCTCTTGGGGAGAGTACCCACTG 222
QY 61 G1yGlnGlnuAspLeuProSerGlnuAspSerProArgGlnuAspProGlyGlnu 80
Db 223 GCGGAGAGAGATTCCTCCAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 282
QY 81 G1uAspLeuProGlyGlnuAspLeuProGlyGlnuAspLeuProGlyValuAspPro 100
Db 283 GAGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCTGAAGTTAAGCT 342
QY 101 LysSerGlnuGlnuGlySerLeuLeuLeuLeuLeuLeuProThrValGlnuAlaProGly 120
Db 343 AAATCAAGAGAGAGAGCTCCCTGAAGTTAGAGATCTACCTGTTGAGGCTCTGGA 402
QY 121 AspProGlnuGlnuProGlnuAspAspAspHisArgAspGlyGlnuAspAspGlnSerHis 140
Db 403 GATCTCAAGAACCCCAAGATTAATCCCAAGAGAGAGAGAGAGAGAGATCAAGAGTCA 462
QY 141 TrpArgTrpGlyGlyAspProProTribProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCGCTATGAGAGGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 522
QY 161 GlnSerProValAspHisArgProGlnuLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCGGAGATATCGGCCCCAGAGCTCGGCTTCTGCCCCGCTGAGCCCCCTG 582
QY 181 G1uLeuLeuGlyPheGlnLeuProProLeuProGlnuLeuArgLeuArgAspAspHis 200
Db 583 GAATCTCCGAGCTTCAAGCTCCGCGCTCCCAAGATCGCGCTGCGCAACATGGCCAC 642
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnuMetAlaLeuGlyProGlyArgGlnuTr 220
Db 643 AGTGTCAACTGACCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
QY 221 ArgAlaLeuGlnLeuHisLeuHisTrpGlyAlaAlaGlyArgProGlySerGlnuHisThr 240
Db 703 CGGGCTCGACAGCTGATCTGACAGGGGGGCTGAGAGTCTGCGGCTCGAGACACT 762
QY 241 ValGlnGlyHisArgPheProAlaGlnuLeuHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGAGAGCCACCGTTTCCCTGCGAGATCCAGTGTCTACCTCAAGACCGCTTTGCC 822
QY 261 ArgValAspGlnuAlaLeuGlyArgProGlyGlnuAlaValLeuAlaAlaPheLeuGlnu 280
Db 823 AGAGTTGACGAGAGCTTGGGGGCGCGGAGAGGCTGCGCGCTTGGCGCTTCTGAG 882
QY 281 G1uGlyProGlnuGlnuAspSerAlaTrpGlnuLeuLeuSerArgLeuGlnuGlnuLeuAla 300
Db 883 GAGGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 942
QY 301 G1uGlnuGlySerGlnuThrGlnuValProGlyLeuAspHisSerAlaLeuLeuProSerAsp 320
Db 943 GAGAGAGCTCAAGAGACTCAAGTCCCAAGACTCAAGTCAAGTCAAGTCAAGTCAAGTCAAG 1002
QY 321 PheSerArgTrpPheGlnuTrpGlnuGlySerLeuThrProProCysAlaGlnuGlnuVal 340
Db 1003 TTCAGCCGCTACTTCAATATGAGGGGCTCTGACTAAGAGAGAGAGAGAGAGAGAGAG 1062

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QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisThrLeuSer 360
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QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnuLeuAspPheArgAlaThrGlnPro 380
Db 1123 GACACCTGTGGGAGCTGTGAGACTCTGCGCTGACAGTGAAGTCTCGAGCGAGAGCT 1182
QY 381 LeuAsnGlyArgValIleGlnuAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1183 TTGAATGGCCAGAGATTTGAGAGCTCTTCCCTGTGAGAGAGAGAGAGAGAGAGAG 1242
QY 401 AlaGlnProValGlnLeuAsnSerCysLeuAlaIleAspHisLeuAlaLeuValPhe 420
Db 1243 GCTAGGCCA-----GGTGAATCTTCAAGCTGCTGTTT 1275
QY 421 G1yLeuLeuPheAlaAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1276 GGCCTCTTTTGGTGTCAACAGAGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1335
QY 441 ArgGlyThrLysGlyGlyValSerTrpArgProAlaGlnuAlaIleGlnuThrGlyAla 459
Db 1336 AGGGGAGACCAAGGGGGTGTGAGCTACCGCCAGAGAGAGTACCGAGACTGAGAGCC 1392

RESULT 5
AL542336
LOCUS
DEFINITION
AL542336 Homo sapiens PLACENTA Homo sapiens cDNA clone CS0DE010YB19
5-PRIME, mRNA sequence.
ACCESSION
AL542336
VERSION
AL542336.3 GI:45717912
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE
1. W.B., Gruber C., Jesse, J. and Polayes, D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On Feb 15, 2001 this sequence version replaced gi:30547384.
COMMENT
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with NotI and cloned
into the NotI and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 8734.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?cs=CS0DE010CA10Q2&c=8734.f.
FEATURES
source
1. 1084
location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CS0DE010YB19"
/tissue_type="PLACENTA"
/clone_lib="Homo sapiens PLACENTA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with NotI and cloned into
the NotI and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
ORIGIN
Alignment Scores:
Pred. No.: 1,64e-134 Length: 1084
Score: 1790.00 Matches: 337
Percent Similarity: 97.99% Conservative: 4

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Db	523	CAGTCCCGGAGATATCCGGCCCGAGTCGGCTTCCTCAGCCGGCCCTGACCCCTG	582
Oy	181	GlutLeuLeuGlyPheGlnLeuProProLeuProGluLeuAglLeuAglAsnAsnGlyHis	200
Db	583	GAACTCCCTGGGGCTTCACACTCCCGCGCTCCAGAACTGCCTGCGCAACAATGGCCAC	642
Oy	201	SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyIyr	220
Db	643	AGTGTGCACACTGACCCCTGCTCTGGGCTTAAGATAGCTCTGGGTCCCGGGCGGAGTAC	702
Oy	221	ArgAlaLeuGlnLeuHisLeuHisITrpGlyAlaAlaGlyArgProGlySerGluHisThr	240
Db	703	CGGGCTTCGACAGCTGACATCTGCACACTGGGGGGCTGCAGGTCGTCCGGGCTCGAAGCACT	762
Oy	241	ValGlnGlyHisArgPheProAlaGlnIleHisValValHisLeuSerThrAlaPheAla	260
Db	763	GTTGAAGGCCACCGTTTCTCCGCGAATCCACGGTGTTCACCTTCAGACCGCTTTGGCC	822
Oy	261	ArgValaIspGluAlaLeuGlyArgProGlyGlyLeuAlaValaAlaPheLeuGlu	280
Db	823	AGAGTTGACGAGGGCTTGGGGCGCCCGGGAAGCCCTGGCGGTGGCC-GCTTTCTGGAG	881
Oy	281	GluGlyProGluGlnAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGluIleAla	300
Db	882	GAGGSGCCGGAAGA-AACAGTGCCTTATAGAGATGGTGTCTCGCTGGGAARA-ATCCT	939
Oy	301	GluGlnGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuPro	318
Db	940	GAGGAAGC-TAGAGACTCAGGKCCAGACTGACAMATT-GCACTCTCTCCT	991
RESULT 8			
LOCUS	BX401186	1017 bp	mRNA linear EST 29-APR-2004
DEFINITION	BX401186 Homo sapiens HELA CELLS COR 25-NORMALIZED Homo sapiens		
ACCESSION	CDNA clone CS0DK009YP10 5-PRIME, mRNA sequence.		
VERSION	BX401186		
KEYWORDS	BX401186.2 GI:46876709		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.		
JOURNAL	1 (bases 1 to 1017)		
COMMENT	Li,W.B., Gruber,C., Jesses,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On May 13, 2003 this sequence version replaced gi:30626393. Contact: Genoscope - Centre National de Sequençage Genoscope - Centre National de Sequençage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by life technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5300.F For more information about this cluster, see http://www.genoscope.cns.fr/cnaTs-CS0DK009DH05QPI&c=5300.F.		

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Location/Qualifiers
1. 1017
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CSDDK009YP10"
/cell_type="HELA CELLS COT 25-NORMALIZED"
/cell_line="HELA"
/clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
note="First strand cDNA was primed with a NotI-oligo (dT)
primer. Five prime end enriched, double-strand cDNA was
digested with Not I and cloned into the Not I and EcoR V
sites of the pCMVSPORT 6 vector. Library was normalized."

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ORIGIN

Alignment Scores:	
pred. No.:	3,44e-111
Score:	1501.50
Percent Similarity:	92.9%
Best Local Similarity:	92.36%
Query Match:	61.94%
DB:	5
Length:	1017
Matches:	290
Conservative:	2
Mismatches:	19
Indels:	4
Gaps:	3

UN-09-967-237A-2 (1-459) x BX041186 (1-1017)

QY	3	ProLeuCyAspSerProThrProThrLeuLeuLeuIleProAlaProAlaProGluLeuThr	22
Db	19	CCCTGTGGCCCAAGCCCTTGGCTCTCTGTGGATCCGGCCCTGTCCAGAGCTTCACT	78
QY	23	ValGlnLeuLeuLeuSerLeuLeuLeuMetProValIleProGlnArgLeuProArg	42
Db	79	GTCGAATGCTGCTGTCACTGCTGCTTCTGTGTGCTGTGTCCATCCCCAGAGTGTGCCCCG	133
QY	43	MetGlnIuAspSerProLeuGlyGlyIleSerSerGlyIuAspAspProLeuGlyGlu	62
Db	139	ATGAGAGAGATTCCCTTGGGAGAGAGCTCTTCTGGGAGAAAGTACCACTGGGCAAG	198
QY	63	GluAspLeuProSerGluGluIuAspSerProArgGluIuAspProProGluGluIuAsp	82
Db	199	GAGGATTTGCCCATGTAAAGAGATTCAACCAAGAGAGATCCACCCGGAGAGAGAT	255
QY	83	LeuProGlyGluGluIuAspLeuProGlyGluIuAspLeuProGluValIleProIleSer	107
Db	259	CTACCTTGAGAGAGAGATCTTACTGGAGAGAGAGATTCTACCTGAAGTTAACTTAATCA	316
QY	103	GluGluGluGlySerLeuLeuIleGluIuAspLeuProThrValGluAlaProGlyIuAspPro	122
Db	319	GAAGAAAGAGGCTTCCCTGAAGTTAGAGATCTAACCCTGTGAGGCTTCTGGAGATCT	378
QY	123	GlnGluProGlnAsnAsnAlaHisArgAspIleGluGlyAspAspGlnSerHisArgArg	144
Db	379	CAGAAGACCCAGAAATATATCCCAACAGGACAAAGAGGAGTACCAAGTCAATTGGCGC	433
QY	143	TyrGlyGlyIuAspProProThrProArgValSerProAlaCysValGlyIuArgPheGlnSer	167
Db	439	TATGGAGGCCAAGCCCGCTTGGCCCGCGGTGTCCCAAGCTGTGGCGCGCGCTTCCAGTCC	498
QY	163	ProValAspIleArgProGlnLeuIuAlaIlePheCysProAlaLeuArgProLeuGluLeu	188
Db	499	CCGGTGGATTCGGCCCCCAAGCTCGCCGCTTCTGTGCGGCCCTGGCCCTCTGGAACTC	558
QY	183	LeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHisSerVal	207
Db	559	CTGGGCTTCCAGCTCCCGCGGCTCCAGAACTGGCGCTGGGCAATATGGCCACAGTGTG	618
QY	203	GlnLeuThrLeuProProGlyIleGluIuMetAlaLeuGlyProGlyIuArgIuThrArgAla	222
Db	619	CAACTGACCTGTGCTCTCTGGGCTAGAGAGGCTGTGGGTCCGGGCGGGAAGTACCGGGCT	678
QY	223	LeuGlnLeuHisIleuHisIleProGlyAlaIleArgIleArgProGlyIleSerGlnHisIleThrValGlu	244
Db	679	CTGCAGCTGATTCGACACTGGGGGCTGAGAGTCTCCGGCTCGAGACACACTGTGAA	733
QY	243	GlyHisIleArgPheProAlaGluIleHisValValHisIleuSerThrAlaPheAlaArgVal	267
Db	739	GGCCACCGTTTCCCTCCAGATCCACGTGTTCACCTCAGCAGCCGCTTTGGCCAGATT	798
QY	263	AspGluAlaLeuGlyIuArgProGlyGlyIleuAlaValIleuAlaIlePheLeuGlnGluGly	288
Db	799	GACGAGGCTTGGGGGGCCCGGAGGCTG-GCCGTGTGGCGCCCTTTTGGAGAGC---	855
QY	283	ProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAlaGluGlu	307
Db	855	CCCGAAGAAACAGTGCCTATAGAGCAG---TTGTGTCTCGCTGWAAGATGCTGAGGAA	911
QY	303	GlySerGluThrGlnValProGlyIleuAspIleSerAlaLeu	316

Db 912 GGT---CAGAGMTCAAGTCCAGACTGGAMTATYTCVTCG 950

RESULT 9
BX423970 916 bp mRNA linear EST 03-MAY-2004
LOCUS BX423970 Homo sapiens NEUROBLASTOMA Homo sapiens cDNA clone
DEFINITION CG0DA003YB12 5-PRIME, mRNA sequence.
ACCESSION BX423970
VERSION BX423970.2 GI:46955310
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
REFERENCE 1 (bases 1 to 916)
AUTHORS Li, W.-B., Gruber, C., Jessee, J. and Polayes, D.
TITLE Full-length cDNA libraries and normalization
JOURNAL Unpublished (2001)
COMMENT On May 15, 2003 this sequence version replaced gi:30766328.
Contact: Genoscope
Genoscope - Centre National de Sequencage
2 rue Gaeleon Cremlieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
This sequence belongs to sequence cluster 5300.f
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna/5-CS1DA001ZFP09QPI&c=5300.f.

FEATURES
Source
1..916
Location/Qualifiers
/organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="CG0DA003YB12"
/issue_type="NEUROBLASTOMA"
/clone_lib="Homo sapiens NEUROBLASTOMA"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."

ORIGIN

Alignment Scores:
Pred. No.: 7,29e-109 Length: 916
Score: 1472.00 Matches: 276
Percent Similarity: 92.43% Conservative: 5
Best Local Similarity: 90.79% Mismatches: 23
Query Match: 60.73% Indels: 0
DB: 5 Gaps: 0

US-09-967-237a-2 (1-459) x BX423970 (1-916)

Qy 1 MetAlaProLeuCyProSerProTrieuProLeuLeu11eProAlaProAlaProGly 20
Db 5 ATGGCTCCCTGTGCTCCCGACGCCCTGCTGTTGAGCCGGGCCCTGCTCCAGGC 64
Qy 21 leuThrAlaGlnLeuLeuLeuSerLeuLeuLeuMetProVal1HlaProGluArgLeu 40
Db 65 CTCACCTGGCAACMGCTGCTCACTGCTGCTTCTGGGCTGTCATCCCAAGAGTTG 124
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 125 CCCCGAGTGAAGAGGAGATTCCCTTGGGAGAGGCTCTWCTGGGGAAGAGACCACTG 184
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 185 GGCAGAGGAGATCTGCCCAAGTGAAGAGATTCAACCAAGAGAGGATCCACCGGAGAG 244
Qy 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluVal1yAspPro 100

Db 245 GAGGATCTACTGGAGAGAGGAGATCTACTGGAGAGGAGATCACTGAAGCTAAAGCT 304
Qy 101 LySerGluGluGluGlySerLeuLeuLeuGluAspLeuProThrVal1GluAlaProGly 120
Db 305 AAATCAGAGAGAGAGGCTCTCTGATAGAGATCTACTGTTGAGGCTCTCGGA 364
Qy 121 AspProGlnGluProGln1naPnaAla1HlaArgAsp1yAspGluGluAspAsp1SerHis 140
Db 365 GAACCTCAAGAACMCACGAATAMGCCACAGGACAAAGAGAGATGACCAAGTCAAT 424
Qy 141 TrpArgTrpGlyGlyAspProProTrieuProArgValSerProAlaCyAlaGlyArgPhe 160
Db 425 TGGCGCATGAGAGCGACCCGCCCTGGCCCGGGTGTACCAAGCTGGGGCGGCTTC 484
Qy 161 GlnSerProValAsp1leArgProGlnLeuAla1aPheCyAspProAlaLeuArgProLeu 180
Db 485 CAGTCCCGGTGGATATCCGCCCCCAAGCTGCGCCCTTGTGCGCGGCTTGGCCCTTG 544
Qy 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 545 GAACCTCTGGGCTTCCAGCTTCCGCCCTCCAGAACCTGGCGCTGGCMACAAATGGCCAC 604
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTrp 220
Db 605 AGTGTGACATGACACCTGCTGCTGCGGCTAGAGMGCTCTGGCTCCGGGCGGAGTAC 664
Qy 221 ArgAlaLeuGlnLeuHis1leuHis1TrpGlyAla1aGlyArgProGlySerGluHisThr 240
Db 665 CGGCTCTGACAGCTGCACTGTGCACTGGGGGCTCAGTCTCGCGGCTCGAGACACACT 724
Qy 241 ValGluGlyHisArgPheProAlaGlu1leHisValValHisLeuSerThrAlaPheAla 260
Db 725 GTGAAAGCCACCGTTTCCGCGCAAGTCCAGTGTTCATACACCGCTTTC 784
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAla1aPheLeuGlu 280
Db 785 ARATTGAMAGAGGCTTGGGGCGCGCGGAGGCTGGCGCGTGGCGGCTTCTTGAG 844
Qy 281 GlyGlyProGluGluAsnSerAla1yGluGlnLeuLeuSerArgLeuGluGluAla 300
Db 845 GAGGCGCCCGGAARAAAATAATCTTARCAATTGCTGTTTCCCTTGGRAAAAMMGT 904
Qy 301 GluGluGlySer 304
Db 905 GAGGAAGCTCA 916

RESULT 10
COS79387 971 bp mRNA linear EST 20-JUL-2004
LOCUS ILUMIGEN_MCO_50239 Katze_MuLi Macaca mulatta cDNA clone
DEFINITION IB1UW:17608 5' similar to Bases 6 to 971 highly similar to human
CA9 (Hs.63287), mRNA sequence.
ACCESSION COS79387
VERSION COS79387.1 GI:50410317
KEYWORDS EST.
SOURCE Macaca mulatta (rhesus monkey)
ORGANISM Macaca mulatta
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
Cercopithecoidea; Macaca.
REFERENCE 1 (bases 1 to 971)
AUTHORS Katze, M.G., Thomas, M., Korth, M., Iadonato, S.P. and Magness, C.L.
TITLE Large-scale Rhesus Macaque cDNA Sequencing
JOURNAL Unpublished (2003)
COMMENT Contact: C. Magness
Illumigen Biosciences Inc.
2203 Airport Way S, Suite 450, Seattle, WA 98134, USA
Tel: 2063780400
Fax: 2063780408
Email: cmagness@illumigen.com
Sequenced on 2004.07.15. 725 Q20 bases. Library Preparation: Prof.
Michael Katze Lab at University of Washington DNA Sequencing:

illumigen Biosciences Inc. For further information, see <http://www.macaque.org>

PCR Primers
 FORWARD: CCTCACTAAAGGAAACAAA
 BACKWARD: CACTATAGGCGCAATTGGCTA
 Insert Length: 971 Std Error: 0.00
 Plate: CL000413 row: A column: 10
 Seq primer: CCTCACTAAAGGAAACAAA
 POLYA=No.

FEATURES
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 /organism="Macaca mulatta"
 /mol_type="mRNA"
 /strain="Indian"
 /db_xref="taxon:9544"
 /clone="IBIUM:17608"
 /sex="male"
 /dev_stage="adult"
 /lab_host="Electromax DH10B"
 /clone_lib="Katz MWIL"
 /note="Organ: ileum; Vector: pDONR 222; Site 1: Berg I; Site 2: Berg I; Created from Cloneminer cdna library construction kit (catalog #18249-029)"

ORIGIN

Alignment Scores:
 Pred. No.: 3e-107 Length: 971
 Score: 1452.50 Matches: 286
 Percent Similarity: 88.92% Conservative: 11
 Best Local Similarity: 85.63% Mismatches: 20
 Query Match: 59.92% Indels: 17
 DB: 7 Gaps: 2

US-09-967-237A-2 (1-459) x COS79387 (1-971)

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QY 55 G|YGLuAspAspProleuG|YGLuAspLeuProSeG|LuAspSerProArgG|u 74
   |||||
Db 3 GGGGAAGATGACCCACATGATGAGAGAGATCTGCCAGTAAAGATCCACAGAGAG 62
   |||||
QY 75 G|UAspProProG|YGLuAspLeuProG|YGLuAspLeuProG|YGLuAsp 94
   |||||
Db 63 GAGAGATCA-----CCAGAGAGAGAT 86
   |||||
QY 95 LeuProG|UValYsProYsSerG|UValYsLeuYsLeuYsLeuYsLeuYsLeu 114
   |||||
Db 87 CTACCTGAAGTAAAGCTTAATCAGAAAGAGAGAGGCTCCCTGAAGTAAAGATCTA 146
   |||||
QY 115 ThValG|UAlaProG|YAspProG|NGLuProG|UAspAsnAlaHisArgAspYsG|u 134
   |||||
Db 147 ACTGTTGAGGCTCTGAGATCTCAAGAACCCAGATATATGCCACAGGAGCAAGAA 206
   |||||
QY 135 G|YAspAspG|NserHisTTPArgY|YGLYAspProProTTPProArgValSerPro 154
   |||||
Db 207 GGGGATTAACAGAGACATCGCCCTATGAGGAGAGAGAGAGAGAGAGAGAGAGAG 266
   |||||
QY 155 AlaCysAlaG|YArgPheG|NserProValAspI|LeuArgProG|NleuAlaAlaPheCys 174
   |||||
Db 267 GCCTGCGCGGCGCTTCCAGTCCCGGATATATCCGCCAGGCTCGCGCTTCTGC 326
   |||||
QY 175 ProAlaLeuArgProleuG|UleuLeuG|YPheG|NleuProProleuProG|UleuArg 194
   |||||
Db 327 CCGGCCCTGGAGCCCTCGAACTCTGGGCTTGAGAGCTCCCGTGTCCCAAGACTGGCG 386
   |||||
QY 195 LeuArgAsnAsnG|YHisSerValG|NleuThLeuProProG|YleuG|UleuAlaLeu 214
   |||||
Db 387 CTGCGCAACAATGCCCACTGCAACTCACTGCTTCGGGCTAGAGATGGCTCTG 446
   |||||
QY 215 G|YProG|YArgG|UValYArgAlaLeuG|NleuHisLeuHisTTPG|YAlaAlaG|YArg 234
   |||||
Db 447 GGTCTCCGCGGAGAGATCAAGGCTCTGAGCTCATCTGAGGAGGCTGTAGGCTGT 506
   |||||
QY 235 ProG|YSerG|UHisThrValG|UValYHisArgPheProAlaG|UleuHisValHis 254
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```

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Db 507 CCGGCTCGGAGACACTGTGAAGGCACCGTTCTTCGCGGAGATCCAGTGTTCAC 566
QY 255 LeuSerThrAlaPheAlaArgValaAspG|UAlaLeuG|YArg-ProG|YleuAlaVa 274
   |||||
Db 567 ATCAGACACCCCTATATGACAGTGTGAAGAGGCTTGGGGGCGCCCGGAGGCTTGGCGCT 626
   |||||
QY 274 LeuAlaAlaPheLeuG|UValYProG|UValYAsnSerAlaTTPG|YLeuLeuLeu 294
   |||||
Db 627 GTTGGCGGCTTCTGAGAGAGGCGCGGAGAAACAGTGCCTATGAGCAGTGTGCTGTC 686
   |||||
QY 294 TArgLeuG|UValYAlaG|UValYSerG|UThrG|NValProG|YleuAspIleu 314
   |||||
Db 687 TCACCTGGAAGAAATGCTGAGAGAGCTCAGACACTCAGCTCCAGAGCTGAGCTATC 746
   |||||
QY 314 TAlaLeuLeuProSerAspPheSerArgY|YPheG|NValYsLeuThrThrPr 334
   |||||
Db 747 TGCACTCGGCGCTTCTGACCTCAAGCGCTACTTCGATATGAGGGGTCTGACTACAG 806
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QY 334 oProCyAlaG|NValYIleTTP-ThrValPheAsnG|NThrValMetLeuSerAla 354
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Db 807 GCCCTGTGCCAGGGGTGTCTATCTGGAGACTGTGTTTACAGACAGATGCTGAGTCTA 866
   |||||
QY 354 YsG|NleuHisThrLeuSerAspThrLeu-TTPG|YProG|YAspSer-ArgLeuG|Nle 373
   |||||
Db 867 ACCACCTCCACCCCTCTCTGAAGCCCTGGGGGAGCTGGGAGCTCTCCGCTTACGGCT 926
   |||||
QY 373 UAspHe-----ArgAlaThrG|NProleuAsnG|Y 383
   |||||
Db 927 GAACCTTCGAGAGAGGAGCCACCTTGGAATGG 960
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```

RESULT 11
 AL55184
 LOCUS
 DEFINITION
 AL55184 Homo sapiens HELA CELLS COT 25-NORMALIZED Homo sapiens
 cDNA clone CSODK007YK10 5-PRIME, mRNA sequence.
 AL55184
 VERSION
 AL55184.3 GI:45859924
 KEYWORDS
 SOURCE
 ORGANISM
 Homo sapiens (human)
 Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
 1 (bases 1 to 927)
 Li, W.B., Gruber, C., Jessee, J. and Polyes, D.
 Full-length cDNA libraries and normalization
 Unpublished (2001)
 On Feb 15, 2001 this sequence version replaced gi:31276993.
 COMMENT
 Contact: Genoscope
 Genoscope - Centre National de Sequenage
 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
 Email: sequef@genoscope.cns.fr, web : www.genoscope.cns.fr
 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
 end enriched, double-strand cDNA was digested with Not I and cloned
 into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library
 was normalized. Library was constructed by Life Technologies, a
 division of Invitrogen. This sequence belongs to sequence cluster
 5300.f
 For more information about this cluster, see
<http://www.genoscope.cns.fr/cdna?c=CSODK007BR05QPlc=5300.f>.

FEATURES
 source 1..927
 /location/Qualifiers
 /organism="Homo sapiens"
 /mol_type="mRNA"
 /db_xref="taxon:9606"
 /clone="CSODK007YK10"
 /cell_type="HELA CELLS COT 25-NORMALIZED"
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 /clone_lib="Homo sapiens HELA CELLS COT 25-NORMALIZED"
 /note="1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."

ORIGIN

Db 773 CTTGCCGAGATCCAGTGTTCACCTCAGACCGCCTTTGCCAGAGTTGACGAGGCGCTTG 714
Qy 267 GtAARProGluYglYleuAlaValAlaAAlaPheLeuGluGluGluYProGluGluAsn 286
Db 713 GGGCGCCCGGAGAGCGCTGCTGTGGCCGCTTTCTGAGAGAGGCGCGGAAAGAAAC 654
Qy 287 SerAlaTyGluGluLeuLeuSerArgLeuGluGluIleAlaGluGluGluSerGluThr 306
Db 653 AGTGCCATGACAGATGGCTCTCCGCTTGGAAGMATCCCTGAGAGAGGCTCAGAGACT 594
Qy 307 GluValProGluLeu--AspIleSerAlaLeuLeu--ProSerAspPheSerArg--TyrPh 325
Db 593 CAGGTCCAGACACTCGGACATCTCTGACCTCCCTGCTCACTTCCAGCCGCGCACTT 534
Qy 325 eGlnTyGluGluYSerLeuThrThrProProCysAlaGlnGluYValIleTrrThrValPh 345
Db 533 CCAATATGAGGGGTCTCTGACTACACCGCCCTGTGGCCAGAGGTGTCATCTGAGCTGTG 474
Qy 345 eAaGlnThrValMetLeuSerAlaYsglnLeuHisThrLeuSerAspThrLeuTrpG1 365
Db 473 TAAACGACACAGTATGCTGAGTCAAGCAGCTCCACACCTCTCTGACACCTGTGGGG 414
Qy 365 YProGluYAspSerArgLeuGluLeuAsnPheArgAlaThrGlnProLeuAsnGluYArgVa 385
Db 413 ACCTGTACTCTCGGCTACAGCTGAACCTCCGAGCGACGAGCTTGAATGGGAGGT 354
Qy 385 lIleGluAlaSerPheProAlaGluYValaAAspSerSerProArgAlaAlaGluProValG1 405
Db 353 GATTGAGGCTCTCTCTGCTGAGAGTGACAGAGAGTCTCGGGCTGTCTAGCGCAAGTCCA 294
Qy 405 nLeuAsnSerCysLeuAlaAlaGluAspIleLeuAlaLeuValaPheGlyLeuLeuPheAl 425
Db 293 GCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 234
Qy 425 aValThrSerValAlaPheLeuValaGlnMetArgArgGlnHisArgArgGlyThrIysG1 445
Db 233 TGTCCACAGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 174
Qy 445 YGluYValSerTyArgProAlaGluValaAlaGluThrGluYAla 459
Db 173 GGGTGTGAGCTACGCGCCAGCAGAGGTAGCGAAACTGGAGCA 131

RESULT 13
Bg386425 874 bp mRNA linear EST 12-MAR-2001
Bg386425 60245652F1 NIH_MGC_15 Homo sapiens cDNA clone IMAGE:458369 5',
LOCUS mRNA sequence.
DEFINITION Bg386425
ACCESSION Bg386425
VERSION Bg386425.1 GI:13279871
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Homnidae; Homo.
1 (bases 1 to 874)
NIH-MGC http://mgi.nci.nih.gov/
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgaabs-remail.nih.gov
Tissue Procurement: ATCC
cDNA Library Preparation: Ling Hong/Rubin Laboratory
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LNL)
DNA Sequencing by: NIH Intramural Sequencing Center
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LNL at:
http://image.llnl.gov
Plate: LNCMI308 row: h column: 14
High quality sequence stop: 714.
Location/Qualifiers
1..874
location="Homo sapiens"
/organism="Homo sapiens"
/mol_type="mRNA"

/db_xref="taxon:9606"
/clone="IMAGE:458369"
/issue_type="adenocarcinoma cell line"
/lab_host="DH10B (phage-resistant)"
/clone_1lb="NIH_MGC_15"
/note="Organ: colon; Vector: pORF7; Site_1: XhoI; Site_2:
EcoRI; cDNA made by oligo-dT priming. Directionally
cloned into EcoRI/XhoI sites using the following 5'
adapter: GGCACTGAG(G). Site-selected >500bp for average
insert size 1.8kb. Library constructed by Ling Hong in
the laboratory of Gerald M. Rubin (University of
California, Berkeley) using Zap-cDNA synthesis kit
(Stratagene) and Superscript II RT (Life Technologies)"

ORIGIN

Alignment Scores:

Pred. No.:	2	5e-95	Length:	874
Score:	1304.50	Matches:	266	
Percent Similarity:	92.15%	Conservative:	4	
Best Local Similarity:	90.78%	Mismatches:	14	
Query Match:	53.82%	Indels:	11	
DB:	4	Gaps:	2	

US-09-967-237A-2 (1-459) x Bg386425 (1-874)

Qy 66 ProSerGluGluAspSerProArgGluGluAspProGluYglYleuAsnLeuProGly 85
Db 2 CCCAGTGAAGAGGATTCACCCAGAGAGAGAGATCCACCGAGAGAGGATCTACCTGGA 61
Qy 86 GluGluAspLeuProGlyGluGluAspLeuProGluValaIlyserGluGluGlu 105
Db 62 GAGGAGAGTCTTACCTGAGAGAGAGATCTACCTGAAGTTAAGCTTAATCAGAAAGAG 121
Qy 106 GlySerLeuYleuGluAspLeuProThrValaGluAlaProGluYAspProGluGluPro 125
Db 122 GGTCTCTGAAAGTTAAGATCTACTACTGTTGAAGCTCTTGAATCTCTCAAGAACCC 181
Qy 126 GlnAsnAsnAlaHisArgAspYsgluGluYAspAspGlnSerHisTrrArgTyGluYglY 145
Db 182 CAGAAATATGCCACAGAGGACAAAGAGGAGATGACACAGATGATGGCGCTATGAGAGGC 241
Qy 146 AspProProTrpProArgValaSerProAlaCysAlaGluYArgPheGlnSerProValaP 165
Db 242 GACCGCGCCCTGGCGCGCGGTGTCCAGGCTGGCGCGGCTTCCAGTCCCGGTGGAT 301
Qy 166 lIleArgProGluLeuAlaAlaPheCysProAlaLeuArgProLeuGluLeuGluYpHe 185
Db 302 ATCCGCGCCAGGTCCCGCTTCTGCTGCGCGCTGCGCGCTGGAATCTCTGGGCTTC 361
Qy 186 GlnLeuProProLeuProGluLeuArgLeuArgAsnGluYHisSerValaGlnLeuThr 205
Db 362 CAGCTCCCGCGCTCCAGAACTGCGCGCTGCGCAATGCGCAAGTGTGCAACTGAGC 421
Qy 206 LeuProProGluYleuGluMetAlaLeuGluYProGluYArgGluYTrpArgAlaLeuGlnLeu 225
Db 422 CTGCTCTCTGGGTAAAGATGCTCTGGGTCCCGGGCGGGAAGTACCGGGCTCTGCAAGCTG 481
Qy 226 HisLeuHisTrrProYValaAlaGluYArgProGlySerGluHisThrValaGluGluYHisArg 245
Db 482 CATCTGACATGGGGGGCTGCAAGTCTCTCGGGCTGGAGCAACATCTGGAAGGCCACCGT 541
Qy 246 PheProAlaGluIleHisValaValHisLeuSerThrAlaPheAlaArgValaAspGluAla 265
Db 542 TTCCCTCGGAGATTCACAGTGGTTCACTCAGACACGCTTTGGCCAGAGTTGACGAGGCC 601
Qy 266 LeuGluYArgProGluYglYleuAlaValaLeuAlaAlaPheLeuGluGluGluYProGluGlu 285
Db 602 TTGGGGCGCGCGGAGATGTGAGAGTGTGGCGCGCTTCTGAGAGA--GGCGCGAAGAGC 660
Qy 286 AsnSerAlaTyGluGluLeuLeuSerArgLeuGluGluIleAlaGluGluGluYserGlu 305
Db 661 AACAGTGCCTTAGAGAGATGCTGTCTCCGCTGGAAGAAATCCCTGAGAGAGGCTCAGAG 720

QY	306	Thr-GlnValPro-GlyLeuAspIleSerAlaLeu-----ProSerAaPheS	322
Db	721	AAATCCAGGGCCCAAGACTGGACATT-----ATCTTGAATCTTGACCTTGTGACTTCA	774
QY	322	eatrGTYr-PheGlnTYrGluGlySer-LeuThrThrProProCybAlaGlnGlyValI1	341
Db	775	AGGGGTACTTCCAAATATAGAGGGGCTCCGGAATACACCGGCTGTGCACAGGGTGTAC	834
QY	341	etTPhrValPheAsnGlnThrValMetLeu 351	
Db	835	CGG-AGTGTGTTACCCAGACATGATGCTT 864	
RESULT 14			
LOCUS	BX383092	836 bp	mRNA
DEFINITION	BX383092 Homo sapiens T CELLS (JURKAT CELL LINE) COT 10-NORMALIZED		
ACCESSION	Homo sapiens cDNA clone CS0DJ005YG10 5-PRIME, mRNA sequence.		
VERSION	BX383092		
KEYWORDS	BX383092.2 GI:46573530		
SOURCE	EST.		
ORGANISM	Homo sapiens (human)		
REFERENCE	Homo sapiens		
AUTHORS	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;		
TITLE	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.		
JOURNAL	1 (base 1 to 836)		
COMMENT	Li,W.B., Gruber,C., Jesse,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001) On May 8, 2003 this sequence version replaced gi:30449113. Contact: Genoscope Genoscope - Centre National de Sequencage 2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr 1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized. Library was constructed by Life Technologies, a division of Invitrogen. This sequence belongs to sequence cluster 5300.f For more information about this cluster, see http://www.genoscope.cns.fr/cdna?e=CS0DJ005BD05QP1&c=5300.f.		
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	/note="1st strand cDNA was primed with a NotI-oligo (dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned into the Not I and EcoR V sites of the pCMVSPORT 6 vector. Library was normalized."		
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Db	100	CTCATCTGTGCAAC	CTGCTGCTGTGCACTGCTGCTTCTGTAAGTCCGTGTCCATCCCAAGAGTTG	155
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Qy	61	GlyglYgluAaspLeuProSerGluInuAaspSerProaGglYgluAaspProGluYglu	80	
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Qy	201	SerValGlnLeuThrlLeuProProGluYleuGluMetAlaLeuGlyProGluYAsGluYur	220	
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ACCESSION	CK971835			
VERSION	CK971835.1			
KEYWORDS	EST.			
SOURCE	Bos taurus (cow)			
ORGANISM	Bos taurus			
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bos.			
AUTHORS	Sonstegard, T.S., Van Tassell, C.P., Matukumalli, L.K., Harhay, G.P., Boeck, S., Rudenfeld, M., and Gasbarre, L.C.			
TITLE	Production of EST from cDNA libraries derived from immunologically activated bovine gut			
JOURNAL	Unpublished (2004)			
COMMENT	Contact: Tad S. Sonstegard Bovine Functional Genomics Laboratory Animal and Natural Resources Institute Bldg. 200 Rm2A BARC-East, Beltsville, MD 20705, USA			

Tel: 3015048416
Fax: 3015048414
Email: cadseanri.barc.usda.gov
Single pass sequencing. Bases called and trimmed with phred
0.000925 using options -trim_alc " -trim fasta. Vector identified
by cross_match using options -trimmatch 12 -minscore 18
Plate: 4 row: M column: 12
Seq primer: CCCAGTCACGACGCTGTAAACG
High quality sequence stop: 740.
Location/Qualifiers

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Site 2: NotI; Equimolar amounts of mRNA extracted from
fundic and pyloric abomasums of 18 and 21 week old steers.
Exposure to Osterlaga osterlagi was initiated at 15 weeks
of age. fundic and pyloric abomasum"

ORIGIN

Alignment Scores:

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US-09-967-237a-2 (1-459) x CK971835 (1-740)

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Db      61  CTCGCCGCACAACTGCGCTGTGCAACACGCGCACACCGCTGACGTGACTG 120
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Db      121  CCTTCCGGGCTGAAGAGCTTGGGCTCCGGGCGAGGATACCGGGCCCTGCAGTTACAT 180
QY      227  LeuHisTrpGlnValAlaAlaGlyArgProGlnSerGlnHisThrValGlnGlnHisArgPhe 246
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Db      181  TTGCACCTGGGGGGCCGGGGTCCGCCGGGCTCGGAACACAGGTTGATGCTCACCGTTT 240
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Search completed: August 20, 2005, 01:25:18
Job time : 4572 secs

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - nucleic search, using frame_p2n model

Run on: August 19, 2005, 22:15:59 ; Search time 887 Seconds

(without alignments)
3361.991 Million cell updates/sec

Title: US-09-967-237A-2

Perfect score: 2424

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BLOSUM62

Xgapop 10.0, Xgapext 0.5

Ygapop 10.0, Ygapext 0.5

Fgapop 6.0, Fgapext 7.0

Delop 6.0, Delext 7.0

Searched: 7316285 seqs, 3248459403 residues

Total number of hits satisfying chosen parameters: 14632570

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-Q=/cgn2_1/USPRO.epool/US09967237/runat_18082005.102620.140/app_query.fasta.1.647

-DB=Published Applications NA -OFMT=fastcap -SUFFIX=p2n.rmpb -MINMATCH=0.1

-LOOPCL=0 -LOOPEXT=0 -UNITS=bites -START=1 -END=-1 -MATRIX=blomsum62

-TRANS=human40.cdi -LIST=45 -DOCALLIGN=200 -THR SCORE=pcc -THR MAX=100

-THR MIN=0 -ALIGN=15 -MODE=LOCAL -OUTFMT=pco -NORM=ext -HEAPSIZE=500 -MINLEN=0

-MAXLEN=200000000 -USER=US09967237@cgn2_1.1480.@runat_18082005.102620.140

-NCPU=6 -ICPU=3 -NO WMAP -LARGECPUERY -NEG SCORES=0 -WAIT -DSBLOCK=100

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and is derived by analysis of the total score distribution.

SUMMARIES

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3	2424	100.0	1522	10	US-09-967-237-1
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5	2424	100.0	1522	21	US-10-888-694-1
6	2424	100.0	1522	21	US-10-921-590-1
7	2424	100.0	1522	22	US-10-723-795-1
8	2424	100.0	1522	9	US-09-954-466-89
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37	1596	65.8	1965	21	US-10-921-590-79
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39	1176.5	48.5	10898	10	US-09-967-237-5
40	1176.5	48.5	10898	21	US-10-888-694-3
41	1176.5	48.5	10898	21	US-10-921-590-3
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43	988	40.8	586	21	US-10-921-590-73
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45	714	29.5	445	10	US-09-967-237-28

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; Sequence 1695, Application US/10102524
; Publication No. US20030109434A1
; GENERAL INFORMATION:
; APPLICANT: Algate, Paul A.
; APPLICANT: Mannion, Jane
; APPLICANT: Gaiger, Alexander
; APPLICANT: Gordon, Brian
; APPLICANT: Harlocker, Susan L.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR THE
; TITLE OF INVENTION: THERAPY AND DIAGNOSIS OF KIDNEY CANCER
; FILE REFERENCE: 210121.572
; CURRENT APPLICATION NUMBER: US/10/102.524
; CURRENT FILING DATE: 2002-03-19
; NUMBER OF SEQ ID NOS: 1863

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; SOFTWARE: FASTSEQ for Windows Version 4.0
; SEQ ID NO 1695
; LENGTH: 1519
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-102-524-1695

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US-09-967-237A-2 (1-459) X US-10-102-524-1695 (1-1519)

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QY      201  SerValGlnLeuThrLeuProProGlyLeuGlnuMetAlaLeuGlyProGlyArgGlyTyr 220
DB      610  AGTGTGAACTGACCCCTGCTCCCGGGCTAGAGATGGCTCTGGGTCCCGGGCGGAGTAC 669
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DB      910  GAGGAGGCTTCAGAGATCGAGTCCAGAGACTGACATATCTGACTCTGCGCTTGAC 969
QY      321  PheSerArgTyrPheGlnuTyrGlnuGlySerLeuThrProProCysAlaGlnuVal 340
DB      970  TTCAAGCGGCTACTTCCATATGAGGGGTCTCTGACTACACCGCCCTGCGCGAGGTGC 1029
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DB      1210  GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1269
QY      421  GlnuLeuPheAlaValThrSerValAlaPheLeuValGlnuMetArgArgGlnuHisArg 440
DB      1270  GGCTCTCTTTTGTGTGACAGAGGTGCTGCTCTCTTGTGAGATGAGAGAGAGAGAG 1329
QY      441  ArgGlyThrArgGlyGlyValSerTyrArgProAlaGlnuAlaGlnuThrArgAla 459
DB      1330  AGGGGAACCAAGGGGTGTGACTACCGGCCAGAGAGGTAGCCAGACTGGAGCC 1386

RESULT 2
US-09-772-719-1
; Sequence 1, Application US/09772719
; Patent No. US20020137910A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Lauder
; STREET: 369 Pine Street
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-JAN-2001
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; APPLICATION NUMBER: US 08/260,190
; FILING DATE: 15-JUN-1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Lauder, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3E
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
```

TELEFAX: 415-981-0332
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1522 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
HYPOTHEICAL: NO
ANTI-SENSE: NO
US-09-772-719-1

Alignment Scores:

Pred. No.:	9,74e-228	Length:	1522
Score:	2424.00	Matches:	459
Percent Similarity:	100.00%	Conservative:	0
Best Local Similarity:	100.00%	Mismatches:	0
Query Match:	100.00%	Indels:	0
DB:	9	Gaps:	0

US-09-967-237a-2 (1-459) x US-09-772-719-1 (1-1522)

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QY 1 MetAlaProLeuCyseProSerProTrieuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCTCCAGCCCTGGCTCCCTGTGATCCCGGCCCTGCTCCAGAGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGCAACTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATCGAGAGAGATTCCTCCCTGGAGAGAGCTCTTCGGGAGAAATACCACTG 192
QY 61 GlyGluGluAspLeuProSerGlyGluAspSerProArgGlyGluAspProProGlyGlu 80
Db 193 GCGCGAGAGATCTGCTCCAGATGAAAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 252
QY 81 GluAspLeuProGlyGlyGluAspLeuProGlyGlyGluAspLeuProGlyValLeuPro 100
Db 253 GAGGATCTACCTCGAGAGAGAGATCTACCTGAGAGAGAGATCTACCTGAAATTAAGCT 312
QY 101 LysSerGlnGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AATATAGAGAGAGAGAGCTCCCTGGAATGAGATCTACCTGCTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspGlyGlyGluAspAspGlnSerHis 140
Db 373 GATCTCTCAAGAAACCCAGAAATATATCCCAAGAGGCAAAAGAGGATGACACAGATCAT 432
QY 141 TrpArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGCCCTATGAGAGGAGCCCGCTGGCCCGCGGCTGCTCCAGCTGGCGGCGGCTTC 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGCTGAGATCCGCCCCCAAGCTCGCGCTCTGCGCGGCCCTGCGGCCCTG 552
QY 181 GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlyHis 200
Db 553 GAACTCTGGGCTTCACAGCTCCCGCGCTCCAGAACTGGCGCTCGCAACAATGGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlnTyr 220
Db 613 AGTGTCAACTGACCTCTCTCTGAGGCTAGAGAGGCTCTGAGGCTCCGGGCGGAGTAC 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisTyrGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CCGGCTCTGCAAGCTGCACTGAGGCGGCTGAGGCTCGTCCGGGCTCGAGCACACT 732
QY 241 ValGluGlyHisArgPheProAlaGluIleHisValAlaHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAGCCCAACCGTTTCCCTGCGAGATTCACGTGTTCACCTCAGCACCGCCCTTTC 792
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QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValAlaLeuAlaPheLeuGlu 280
Db 793 AGAGTTGACAGAGCCCTTGGGCGCCCGGAGAGCCCTGCGCTGTGGCCCTTTCTGAG 852
QY 281 GlnGlyProGlnGluAsnSerAlaTyrGlnLeuLeuSerArgLeuGlnGluAla 300
Db 853 GAGGGCCCGGAGAAACAGTGCCATATGACAGTTGCTGTCTCGCTGGAAGAAATCCCT 912
QY 301 GlnGluGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGCTCAGAGACTCAGGTCCAGACTGACATATCTGCACTCTCCCTCTAC 972
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTCACCCCTCTCTTCAATATGAGGAGTCTCTGACTACACCGCCCTGTGCCAGGCTTC 1032
QY 341 IleThrThrValPheAsnGlnThrValMetLeuSerAlaGlyGlnLeuHisThrLeuSer 360
Db 1033 ATCTGACATGTTTAAACAGACAGTATGCTGAGTGTAAAGCAGCTCCACACCTCTCT 1092
QY 361 AspThrLeuTyrGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAGCTGTGACTCTCGCTACAGCTGAACCTTCGAGCAGCAGAGCT 1152
QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGCCAGATGATTAAGAGCTCTCTCTCTGAGAGTGCAGAGAGATCTCGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTGTGCTGACACAGGCTGCTCTCTGTCAGATGAGAGAGCAGACAGA 1332
QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db 1333 AGGGAAACCAAGGGGCTGTGACTACCGCCAGCAGAGGTAGCCAGACTGGAGCC 1389
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RESULT 3
US-09-967-237-1
Sequence 1, Application US/09967237
Publication No. US20030049826A1
GENERAL INFORMATION:
APPLICANT: Zavada, Jan
APPLICANT: Pastorekova, Silvia
APPLICANT: Pastorek, Jaromir
TITLE OF INVENTION: NM Gene and Protein
FILE REFERENCE: D-0021.58-2
CURRENT APPLICATION NUMBER: US/09/967,237
PRIOR FILING DATE: 2001-09-27
PRIOR APPLICATION NUMBER: 09/178,115
NUMBER OF SEQ ID NOS: 116
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 1
LENGTH: 1522
TYPE: DNA
ORGANISM: HUMAN
FEATURE:
NAME/KEY: CDS
LOCATION: (13)..(1389)
NAME/KEY: mat_peptide
LOCATION: (124)..(1389)
US-09-967-237-1

Alignment Scores:
Pred. No.: 9,74e-228 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0

Query Match: 100.00% Indels: 0
 DB: 10 Gaps: 0
 US-09-967-237A-2 (1-459) x US-09-967-237-1 (1-1522)

QY 1 MetAlaProLeuCySProSerProTIPLeuProLeuLeuIleProAlaProGly 20
 DB 13 ATGGCTCCCTGTGCCCCAGCCCTCGCTCCCTGTGATCCCGGCCCTGCTCCAGGC 72
 QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
 DB 73 CTCACCTGTCACTGCTGCTGTCTGCTGCTGTGATGCTGTGCTTCCATCCCAAGGTTG 132
 QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
 DB 133 CCCCAGATGAGAGAGATTCCCCCTTGAGAGAGGCTCTTGCGGGAAGATGACCACTG 192
 QY 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProGlyGlu 80
 DB 193 GGCAGAGAGATCTGCCAGTGAAGAGATTCAACCCAGAGAGAGATCCACCCGAGAG 252
 QY 81 GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGlyValLeuPro 100
 DB 253 GAGGATTTACTGAGAGAGAGATCTTACTGAGAGAGATCTTACTGATTAAGTTAACCT 312
 QY 101 LysSerGluGluGluGlySerLeuLeuLeuGluAspLeuProThrValGluAlaProGly 120
 DB 313 AAATCAGAAAGAGGGCTCCCTGAGATTAGAGATCTTACTGATTGAGGCTCCTGGA 372
 QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGluAspAspGlnSerHis 140
 DB 373 GATCTCTAAGAAACCCAGAAATAAGCCACAGGAGCAAGAGGATGACCAAGATCAT 432
 QY 141 TrpArgTyrGlyGlyAspProProTIPProArgValSerProAlaCysAlaGlyArgPhe 160
 DB 433 TGGCGCTATGAGAGCGACCCGCCCTGGGCCCGGGGTGTCCAGGCTCGGGCGCGCTTC 492
 QY 161 GlnSerProValAspLeaArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
 DB 493 CAGTCCCCGGGTGATATCCGCCCCAGCTCGGCCCTTGTGCCGGCGCCGCCCTG 552
 QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuAlaGlnAsnGlyHis 200
 DB 553 GAATCTCTGGGCTTCCAGCTCCGCCCTCCCAAACTGGCGCTCCCAACAAGGGCCAC 612
 QY 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyTyr 220
 DB 613 AGTGTGAACTGACCTTGCTCTCTGGGCTAGAGATGGCTTGGGTCCCGGGCGGAGTAC 672
 QY 221 ArgAlaLeuGlnLeuHisLeuHisSerGlyValAlaGlyArgProGlySerGlnHisThr 240
 DB 673 CGGGCTGTGACGTGATCTGCACTGGGGGGCTGCAAGTGGCTCGGGCTCGAGACACT 732
 QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisValValHisLeuSerThrAlaPheAla 260
 DB 733 GTGAAAGCCACCGTTTCCCTGCGCAATCCACGTGTTCACCTGACACCGGCTTTGGC 792
 QY 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
 DB 793 AGAGTTGACAGAGCTTGGGGCGCCCGGAGGCTTGCCGTGGCGCTTTCGAG 852
 QY 281 GlyGlyProGluGluAsnSerAlaTyrGluGlnLeuLeuSerArgLeuGluGluIleAla 300
 DB 853 GAGGGCCCGAAGAAAACAGTGCCTATGACAGATTGCTGTGCTTGGAAAGAAATGCT 912
 QY 301 GluGlnGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
 DB 913 GAGGAAGCTCAGAGACTCAGGTCCTCCAGACTGAGATATCTGACTCCGCTTGAC 972
 QY 321 PheSerArgTyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
 DB 973 TTCAAGCCGCTACTTCCAAATATGAGGGGTCTGTGACTACCGCCCTGTGCCAGGGGTGC 1032

QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisSerThrLeuSer 360
 DB 1033 ATCTGACCTGTGTTAAACAGACAGATGCTGAGTGTAAAGAGCTCCACACCTCTCT 1092
 QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
 DB 1093 GACACCTGTGGGACCTGTGTGACTCTGGCTACAGTGAATCTCCAGAGAGAGGCT 1152
 QY 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
 DB 1153 TTGAATGGGAGATGATGAGGCTCTCTCCCTGCTGAGTGAACAGACATCTCGGGCT 1212
 QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLeuAlaValPhe 420
 DB 1213 GCTGAGCCAGTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
 QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
 DB 1273 GGCCTCTTTTCTGTGACACAGCGTGCCTTCTTGTGAGATGAGAGAGACACAGA 1332
 QY 441 ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
 DB 1333 AGGGAAACCAAGGGGTGTGAGCTTACCGCCAGCAGAGGTACCGAGCTGAGGCC 1389

RESULT 4 US-10-795-933-5 Sequence 5, Application US/10795933 Publication No. US20040259126A1 GENERAL INFORMATION:

APPLICANT: Zavada, Jan
 APPLICANT: Pastorek, SIlvIa
 APPLICANT: Pastorek, JaromIir
 TITLE OF INVENTION: MN Gene and Protein
 FILE REFERENCE: D-0021-2
 CURRENT APPLICATION NUMBER: US/10/795, 933
 CURRENT FILING DATE: 2004-03-08
 PRIOR APPLICATION NUMBER: US/08/260, 190
 PRIOR FILING DATE: 1994-06-15
 PRIOR APPLICATION NUMBER: 08/177, 093
 PRIOR FILING DATE: 1993-12-30
 PRIOR APPLICATION NUMBER: 07/964, 589
 PRIOR FILING DATE: 1992-10-21
 PRIOR APPLICATION NUMBER: PV-709-92
 PRIOR FILING DATE: 1992-03-11
 NUMBER OF SEQ ID NOS: 26
 SOFTWARE: PatentIn Ver. 2.0
 SEQ ID NO 5
 LENGTH: 1522
 TYPE: DNA
 ORGANISM: HUMAN
 FEATURE:
 NAME/KEY: CDS
 LOCATION: (13) .. (1389)
 FEATURE:
 NAME/KEY: mat_peptide
 LOCATION: (124) .. (1389)
 US-10-795-933-5

Alignment Scores:

Pred. No.: 9 74e-228 Length: 1522
 Score: 2424.00 Matches: 455
 Percent Similarity: 100.00% Conservative: 0
 Best Local Similarity: 100.00% Mismatches: 0
 Query Match: 100.00% Indels: 0
 DB: 20 Gaps: 0

US-09-967-237A-2 (1-459) x US-10-795-933-5 (1-1522)

QY 1 MetAlaProLeuCySProSerProTIPLeuProLeuLeuIleProAlaProGly 20
 DB 13 ATGGCTCCCTGTGCCCCAGCCCTGCTGCTCTTGTGATCCCGGCCCTGCTCCAGGC 72
 QY 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40

Db	73	CTACACTGTGAACTGCTGCTGTGTCACTGCTCTTCTGATGCTCTTCCATCCCAAGAGTTG	132
QY	41	ProArgMetGlnGluAspSerProLeuGlyGlyIysSerSerGlyGluAspAspProLeu	60
Db	133	CCCCGATGACAGAGGATTCCTCCCTTGGAGGAGGCTCTTCTGCGGGAAGATGACCACTG	192
QY	61	GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu	80
Db	193	GGGAGAGAGGATCTGCCACTGAAAGAGATTCACCCAGAGAGAGGATTCACCCGGAGAG	252
QY	81	GluAspLeuProGlyGluGluAspLeuProGlyGluGluAspLeuProGluValIysPro	100
Db	253	GAGGATCTTACTGAGAGAGAGATCTTACTTGGAGAGAGATCTTACTGAGATTAAAGCTT	312
QY	101	LysSerGluGluGluGlySerLeuLysLeuGluAspLeuProThrValGluValProGly	120
Db	313	AAATTCAGAAAGAGGGCTCTCCGAAATTGAGAGATCTACTCTTTGAGGCTCTCGA	372
QY	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGluGlyAspAspGlnSerHis	140
Db	373	GATCCCTCAAAACCCCAAGATTAATGCCACAGGAGCAAAAGAGGGATGACCAAGATCTAT	432
QY	141	TrpArgTrsGlyGlyAspProProProProArgValSerProAlaCysAlaGlyArgPhe	160
Db	433	TGGCGCTATGAGAGCCAGCCCGCTGGCCCCGGGGTGTCCCACTGCGGGGGCGCTTC	492
QY	161	GlnSerProValAspIleArgProGlnLeuValAlaPheCysProAlaLeuArgProLeu	180
Db	493	CAGTCCCGGTGATATCCGCCCCCAAGCTGCGCGCTTCTGCGCGGCGCTGCGCCCTG	552
QY	181	GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnAsnGlyHis	200
Db	553	GAACTCTTGCGCTTCCAGCTCCCGCGCTCCCAAGACTGGCGCTCGCAACATGGCCAC	612
QY	201	SerValGluLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyIhrArgIuTr	220
Db	613	AGGTGCAATGACCTGCTCTCTGGAGTAAAGATGATCTCTGGGTCCCGGCGGGATAC	672
QY	221	ArgAlaLeuGlnLeuHisLeuHisIstProGlyAlaAlaGlyArgProGlySerGluHisThr	240
Db	673	CGGGCTCTGAGTGCATCTGCATCTGGGGGGCTGCAGTGTCTCCGGGCTCGAGACACT	732
QY	241	ValGluGlyHisArgPheProAlaGluIleHisValValHisLeuSerThrAlaPheAla	260
Db	733	GTCGAGAGCCACCGTTTCCCTGCGGAGATCCAGTGATTCACCTCGACACCGGCTTTGCC	792
QY	261	ArgValAspGluAlaLeuGlyArgProGlyGlyLeuValValLeuAlaAlaPheLeuGlu	280
Db	793	AGAGTTGACAGAGGCTTGGGGCCCGGGAGGCTGGCGGTGTGGCCGCTTTTCGGAG	852
QY	281	GluGlyProGluGluAsnSerAlaTrpGluGluLeuLeuSerArgLeuGluIleAla	300
Db	853	GAGGGCCCGGAGAAACAGTGCCTTATGACGATTGCTGTCTGCTTGGAGAAATCGCTT	912
QY	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	913	GAGGAAGGCTCAGAGACTCAGGTCCAGAGACTGACATATCTGCACTCTCGCCCTTGAC	972
QY	321	PheSerArgTrpPheGlnTrpGluGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	973	TTCAAGCCGCTACTTCAMATATGAGGGGTCTCTGACTACACCGGCTGTCCAGAGGTGTC	1033
QY	341	IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGluLeuHisIsthrLeuSer	360
Db	1033	ATTGGAATCTGTATTAAACAGACAGATGCTGATGAGTCTAAAGCACTCCACACCTCTCT	1093
QY	361	AspThrLeuTrpGlyProGlyAspSerArgLeuGluLeuAsnPheArgIleThrGlnPro	380
Db	1093	GACACCTGTGGGAGCTGGTGACTCTCGGCTACACTGAATTCGAGACGACGAGCTT	1153
QY	381	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla	400

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Db      1153  TTGAATGGGCGAGGATTGAGAGCCTCTCTCCCTGCTGGAGTGGACAGACAGTCTCGGCT 1212
Qy      401    AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db      1213  GCTGAGCCAGTCCAGCTGAATTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1272
Qy      421    GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnmCtArgArgGlnHisArg 440
Db      1273  GGCCTCCTTTTGTGCTGCACACGAGGTGCGCTTCCTGTGCAGAAAGAGAAAGGCACACAGA 1332
Qy      441    ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla 459
Db      1333  AGGGGACCAAGGGGGGTGTAGCTACCGCCACAGACAGGTAGCCGAGACTGGAGCC 1389

RESULT 5
US-10-888-694-1
; Sequence 1, Application US/10886694
; Publication No. US20050003425A1
; GENERAL INFORMATION:
; APPLICANT: Zavada, Jan
; Pastorekova, Silvia
; Pastorek, Jaromir
; TITLE OF INVENTION: MN Gene and Protein
; NUMBER OF SEQUENCES: 86
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Leona L. Laufer
; STREET: 465 California Street, Suite 450
; CITY: San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94104
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/10/888,694
; FILING DATE: 08-Jul-2004
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/09/772,719
; FILING DATE: 30-Jan-2001
; APPLICATION NUMBER: US 08/485,049
; FILING DATE: 07-JUN-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Laufer, Leona L.
; REGISTRATION NUMBER: 30,863
; REFERENCE/DOCKET NUMBER: D-0021.3A-2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415-981-2034
; TELEFAX: 415-981-0332
; INFORMATION FOR SEQ ID NO: 1:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 1522 base pairs
; TYPE: nucleic acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: cDNA
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; SEQUENCE DESCRIPTION: SEQ ID NO: 1:
US-10-888-694-1

Alignment Scores:
Pred. No.:      9.74e-228      Length:      1522
Score:          2424.00      Matches:      459
Percent Similarity: 100.00%      Conservative: 0
Best Local Similarity: 100.00%      Mismatches: 0
Query Match:     100.00%      Indels:      0
DB:              21          Gaps:        0

US-09-967-237A-2 (1-459) x US-10-888-694-1 (1-1522)

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QY 1 MetAlaProLeuCySProSerProTribLeuProLeuLeu1leProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCTCCCGAGCCCTGGCTCCTGTGTAATCCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrAlaGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACTGTGAAACGCTGCTGTCACTGCTGCTGTGATGCTGCTCCATCCCAAGGATTG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlyYSerSerGlyGluAspAspProLeu 60
Db 133 CCCCAGATGCAAGAGGATTCCTCCCTTGGAGAGAGGCTTCTTGGGGAAGATGACCACTG 192
QY 61 GlyGluGluAspLeuProSerGlyGluAspSerProArgGlnGluAspProProGly 80
Db 193 GGCAGAGAGATGCCCCAGTGAAGAGATTCACCAGAGAGAGATTCACCCGAGAG 252
QY 81 GluAspLeuProGlyGlyGluAspLeuProGlyGlyGluAspLeuProGlyValLeuPro 100
Db 253 GAGGATCTACCTGGAGAGAGATCTACCTGGAGAGAGATCTACCTGAAGTTAACCTT 312
QY 101 LysSerGlnGluGlnGlySerLeuLysLeuGluAspLeuProThrValGluAlaProGly 120
Db 313 AAATCAGAAAGAGGCTCCTGTAAGTGAAGATCTACTGTTGAGGCTCTCTGGA 372
QY 121 AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAACCCGAGAAATATGCCCACAGGGACAAGAGGATGACAGAGATCAT 432
QY 141 TTPArgTyrGlyGlyAspProProTyrProArgValSerProAlaCysAlaGlyArgPhe 160
Db 433 TGGGCTATGAGAGCGACCCGCTGAGCCCGGGTGTGCCACAGCTTCGGGGCGGCTTC 492
QY 161 GlnSerProValAspLeaArgProGlnLeuAlaIlePheCysProAlaLeuAspProLeu 180
Db 493 CAGTCCCGGGTGAATACCGCCCGACAGCTGGCGCTTCGCCGGCGCTGCGGCCCTG 552
QY 181 GlnLeuLeuGlnPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnArgHis 200
Db 553 GAACCTCTGGGCTTCAGAGCTCCGCGCTCCAGAACTGGCGCTCGGCACAAATGAGCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlyTyr 220
Db 613 AGTGTGCACTGACCTGCTGCTGCTGAGAGTGTGCTGCTGCTGCTGCTGCTGCTGCTG 672
QY 221 ArgAlaLeuGlnLeuHisLeuHisIleTrpGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 673 CGGGCTTGCAGCTGCACTGCACTGGGGGGCTGCAAGTGTGCTCGGGCTCGAGACACT 732
QY 241 ValGlnGlyHisArgPheProAlaGlnIleHisValValHisLeuSerThrAlaPheAla 260
Db 733 GTGGAAAGGCACCGTTTCCCTGCGAGATCCAGTGTGTTCACTCAGACACCGCTTGGC 792
QY 261 ArgValAlaAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTGACAGAGCTTGGGGCGCGCGAGAGCTGCGCTGTTGGCGGCTTCTGAGAG 852
QY 281 GlnGlyProGlnGluAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGluIleAla 300
Db 853 GAGGGCCCGGAAGAAACAGTGTCTATGACAGATGCTGTCTGCTGCTGGAAGAAATGCT 912
QY 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAAGGCTCAGAGACTCAGGTCCAGAGACTGGAATATCTGACTCTGCTCTGAC 972
QY 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 973 TTGAGCGGCTACTTCAATATGAGGGGTCTCTGATCAACCGCTGTGCGCAGGGGTCT 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisIleLeuSer 360
Db 1033 ATCTGAGCTGTGTTTAACAGACAGATGCTGAGTGTCTAAGCAGCTCCACACCTCTCT 1092
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QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGGAAGCTGTGACTCTCGGCTACAGCTGAATCTCCGAGCGCAGCCCT 1152
QY 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerProAlaGlyAla 400
Db 1153 TTGAATGGCGAGATGAGTGGGCTCTCTTCCCTGCTGAGTGAACAGCATCTCGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGGCACTCCAGCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
QY 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetCysArgGlnHisArg 440
Db 1273 GGCCTCTTCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1332
QY 441 ArgGlyThrIleGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
Db 1333 AGGGAACCAAGAGGGGTGTGACTACCGCCAGCAGAGGTAGCCAGACTGAGACC 1389

RESULT 6
US-10-921-590-1
; Sequence 1, Application US/10921590
; Publication NO. US20050031623A1
; GENERAL INFORMATION:
; APPLICANT: Pastorex, Jaxomix
; APPLICANT: Zavada, Jan
; APPLICANT: Ortova Gut, Marta
; APPLICANT: Zatorovicova, Silvia
; APPLICANT: Pastorekova, Silvia
; TITLE OF INVENTION: SOLUBLE FORM OF CARBONIC ANHYDRASE IX (s-CA IX), ASSAYS TO DETECT
; TITLE OF INVENTION: s-CA IX, CA IX's COEXPRESSION WITH HER-2/neu/c-erbB-2 AND CA
; FILE REFERENCE: MST-2363/2376 US
; CURRENT APPLICATION NUMBER: US/10/921, 590
; CURRENT FILING DATE: 2004-08-19
; PRIOR APPLICATION NUMBER: 60/358, 824
; PRIOR FILING DATE: 2002-02-21
; PRIOR APPLICATION NUMBER: 60/383, 068
; PRIOR FILING DATE: 2002-05-23
; PRIOR APPLICATION NUMBER: 60/431, 499
; PRIOR FILING DATE: 2002-12-05
; PRIOR APPLICATION NUMBER: PCT/US03/05136
; PRIOR FILING DATE: 2003-02-21
; PRIOR APPLICATION NUMBER: PCT/US03/05137
; PRIOR FILING DATE: 2003-02-21
; NUMBER OF SEQ ID NOS: 118
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13) .. (1389)
; FEATURE:
; NAME/KEY: mat peptide
; LOCATION: (124) .. (1389)
; US-10-921-590-1

Alignment Scores:
Pred. No.: 9, 74e-228 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 21 Gaps: 0

US-09-967-237A-2 (1-459) x US-10-921-590-1 (1-1522)
QY 1 MetAlaProLeuCySProSerProTribLeuProLeuLeu1leProAlaProAlaProGly 20
|||||
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13 ATGGCTCCCTGTGCCCCAGCCCTTGCTCCCTCTTGATCCCGGCCCTGCTCCAGGC 72
QY LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 21
73 CTCACGTGCACTGCTGTCACGTGCTTCGATCCGTGTCATCCAGAGTTGG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGlyuAspAspProLeu 60
Db 133 CCCCAGATGCAGAGAGATTTCCCTTGGAGAGAGCTCTTCTGGGGAAATATACCACTG 192
QY 61 GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
Db 193 GCGCAGAGAGATCTGCCAGATGATTCACCAAGAGAGATTCACCCGAGAG 252
QY 81 GlnuAspLeuProGlyGlnGluAspLeuProGlyGlnGluAspLeuProGlyuAspPro 100
Db 253 GAGGATCTCACTGAGAGAGAGATCTCACTGAGAGAGAGATCTCACTGAAATTAAAGCT 312
QY 101 LysSerGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGlnuAspProGly 120
Db 313 AAATCAGAAAGAGAGAGCTCCCTGAAATTAGAGATCTACTGTTGAGGCTCTGGA 372
QY 121 AspProGlnGluProGlnuAspAsnHisHisArgAspLysGlnGlyAspAspGlnSerHis 140
Db 373 GATCCTCAAGAAACCCAGATATATGCCCAAGAGAAAGAGAGATGACAGAGTCA 432
QY 141 TPATGTYTGYLYGlyAspProProTrpProArgValSerProAlaCysAlaIleArgPhe 160
Db 433 TGGCCCTATGAG 492
QY 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 493 CAGTCCCGGTGAGATTCGCCCCCAAGCTCGCCGCTTCTGCCCCGAGAGAGAGAGAG 552
QY 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnGlyHis 200
Db 553 GAATCCTGAGGCTTCCAGCTCCGCGGCTCCAGAACTGCGCTGGCGGCAATGAGCCAC 612
QY 201 SerValGlnLeuThrLeuProProGlyLeuGlnuMetAlaLeuGlyProGlyArgGlyuArg 220
Db 613 AGTGTCAACTGACCTGCTCTCTGAGCTGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 672
QY 221 ArgAlaLeuGlnLeuHisIleuHisIleuHisIleuHisIleuHisIleuHisIleuHis 240
Db 673 CGGAGCTGCACTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 732
QY 241 ValGlnGlyHisArgPheProAlaGlnuIleHisValHisIleuSerThrAlaPheAla 260
Db 733 GTGGAAGGCCACCGTTCCCTGCGAGATCCAGTGTTCACCTCAGCACCGCCTTTGCG 792
QY 261 ArgValAspGlnuAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 793 AGAGTTCAGAGAGCTTGGGGGCGCCGAGAGAGAGAGAGAGAGAGAGAGAGAGAGAG 852
QY 281 GlnGlyProGlnGluAsnSerAlaTyrglnGlnLeuLeuSerArgLeuGlnGluIleAla 300
Db 853 GAGGGCCCGGAAGAAACAGTCCCTHAGAGCACTGCTGCTGCTGCTGCTGCTGCTGCT 912
QY 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 913 GAGGAAGGCTCAGAGACTCAGGCTCCAGAGACTGACATATCTGCACTCCTGCTCTAC 972
QY 321 PheSerArgTyrgPheGlnTyrglnGlySerLeuThrTrpProProCysAlaGlnuIleVal 340
Db 973 TTCAGCCCTACTTCCATATGAGAGAGGCTCTGACTACCGCCTGTGGCCAGAGGTTC 1032
QY 341 IleTrpThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisIleuLeuSer 360
Db 1033 ATCTGCACTGTGTTAAACAGCACTGATGCTGATGCTGATGCTGATGCTGATGCTGAT 1092
QY 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1093 GACACCTGTGGGAG 1152

QY 381 LeuAsnGlyArgValIleGlnuAspPheProAlaGlyValAspSerSerProArgAla 400
Db 1153 TTGAATGGGCGAGATATGAGGCTTCTTCTGCTGAGATGAGACAGCTGCTGGGCT 1212
QY 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1213 GCTGAGCCAGTCTCAGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
QY 421 GlyLeuLeuPheAlaValHisSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTGTGCTGACAGCGCTCGCTTCTTGTGCAATGATGAGAGCAGACAGA 1332
QY 441 ArgGlyThrLysGlyValSerTyrgPheProAlaGlnuValAlaGlnuThrGlyAla 459
Db 1333 AGGGGAACCAAGGGGGTGTGAGTACCGCCAGCAGAGATGACCGAGACTGGAGCC 1389

RESULT 7
US-10-723-795-1
; Sequence 1, Application US/10723795
; Publication No. US20040146955A1
; GENERAL INFORMATION:
; APPLICANT: Supuran, Claudiu
; APPLICANT: Scozzafava, Andrea
; APPLICANT: Pastorekova, Silvia
; APPLICANT: Pastorek, Jaromir
; TITLE OF INVENTION: CA IX-SPECIFIC INHIBITORS
; FILE REFERENCE: MST-2393 US
; CURRENT APPLICATION NUMBER: US/10/723,795
; PRIOR FILING DATE: 2003-11-26
; PRIOR APPLICATION NUMBER: 60/429,089
; PRIOR FILING DATE: 2002-11-26
; PRIOR APPLICATION NUMBER: 60/489,473
; PRIOR FILING DATE: 2003-07-22
; PRIOR APPLICATION NUMBER: 60/515,140
; PRIOR FILING DATE: 2003-10-28
; NUMBER OF SEQ ID NOS: 9
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 1
; LENGTH: 1522
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (13)..(1389)
; FEATURE:
; NAME/KEY: mat_peptide
; LOCATION: (124)..(1389)
US-10-723-795-1

Alignment Scores:
Pred. No.: 9,74e-228 Length: 1522
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
DB: 22

US-09-967-237a-2 (1-459) x US-10-723-795-1 (1-1522)

QY 1 MetaLapLeuAspProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly 20
Db 13 ATGGCTCCCTGTGCCCCAGCCCTTGCTCCCTCTTGATCCCGGCCCTGCTCCAGGC 72
QY 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 73 CTCACGTGCACTGCTGTCACGTGCTTCGATCCGTGTCATCCAGAGTTGG 132
QY 41 ProArgMetGlnGluAspSerProLeuGlyGlySerSerGlyGlyuAspAspProLeu 60
Db 1213 GCTGAGCCAGTCTCAGCTGATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 1272
QY 421 GlyLeuLeuPheAlaValHisSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1273 GGCCTCTTTTGTGCTGACAGCGCTCGCTTCTTGTGCAATGATGAGAGCAGACAGA 1332
QY 441 ArgGlyThrLysGlyValSerTyrgPheProAlaGlnuValAlaGlnuThrGlyAla 459
Db 1333 AGGGGAACCAAGGGGGTGTGAGTACCGCCAGCAGAGATGACCGAGACTGGAGCC 1389

QY 61 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 133 GACACCTGTGGGAG 1152

Dp	193	GGCGAGAGAGATCTGCCAGTGAAGGATTACCCAGAGAGAGATCCACCGGAGG	252
Qy	81	GlusAspLeuProGluYgluIuAspLeuProGlyGluIuAspLeuProGluValIysPro	100
Dp	253	GAGAGTCTACCTGGAGAGGAGGATCTACCTGGAGAGGAGGATCTACCTGAATTAAAGCCT	312
Qy	101	LysSerGluGluGluGlySerLeuYleLeuGluAspLeuProThrValIgluAlaProGly	120
Dp	313	AAATCAGAGAGAGAGGCGCTCCCTGGAAGTTAGAGGATCTACTTACCTTGAAGGCTCTTGGA	372
Qy	121	AspProGluIuProGluIuAsnAsnAlaHisArgAspIysGluGlyAspAspGlnSerHis	140
Dp	373	GATCTCCAGAAACCCCGAATATATGCCACAGAGAGCAAAAGGGGATACCAAGATCAAT	432
Qy	141	TrpArgIyrGlyGlyAspProProTrpProArgValSerProAlaCysAlaIylArgPhe	160
Dp	433	TGGCGCTATGAGAGGGGACCCCGCCTGGCCCGGGGTGTCCCAAGCTCGCGCGGCGCTTC	492
Qy	161	GlnSerProValAspIleArgProGluIuAlaAlaPheCysProAlaLeuArgProLeu	180
Dp	493	CAGTCCCGAGTGAATCCGCCCCAGCTCGCGCCTTGTGCGCGGCTCGGCGCCCTG	552
Qy	181	GluLeuLeuGlyPheGluIuLeuProProIuProGluIuLeuArgLeuArgAsnGlnHis	200
Dp	553	GAACTCCGAGGCTTCAGCTCCGCGCGCTCCAGAACTGCGCTGGCAACATGGCCAC	612
Qy	201	SerValGlnLeuThrLeuProProGlyLeuGluIuMetAlaLeuGlyProGlyArgIuIyr	220
Dp	613	AGTGTGCAACTGACCTCGCTCTGGGCTAGAGATGGCTCTGGGTCCGGGGGGAGTAC	672
Qy	221	ArgAlaLeuGluIuLeuHisIleuHisTrpGlyAlaAlaGlyArgProGlySerGluHisTr	240
Dp	673	CGGGCTCTGACGCTCATCTGCACCTGGGGGGCTGCAGGCTGCTCGGGCTCGAGGACACT	732
Qy	241	ValGluGlnHisArgPheProAlaGluIuIleHisValHisIleuSerThrAlaPheAla	260
Dp	733	GTGGAAGGCCACCGTTCCCTGCGCAGAGATCCAGTGTTCACCTCAGCACCGCTTTGGC	792
Qy	261	ArgValaAspGluAlaLeuGluYArgProGlyGlyLeuAlaValIleuAlaAlaPheLeuGlu	280
Dp	793	AGAGTGAACGAGGCTTGGGGGGCGCCGGAGAGGCTGGCGGTGTGGCGCCTTCTCGAG	852
Qy	281	GluGlyProGluGluIuAsnSerAlaTyrGluIuLeuLeuSerArgLeuGluGluIuIleAla	300
Dp	853	GAGGGCCCGAAGAAACAGTCCATGAGCGATGTGCTGTCTGCTTGGAAAGAAATCGCT	912
Qy	301	GluGluGlySerGluThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerArg	320
Dp	913	GAGGAAGGCTCAGAACTCAGGTCCCGAGGACTGGAATATGCACTCTGCGCTCTTGAC	972
Qy	321	PheSerArgIyrPheGlnTyrGluGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Dp	973	TTCAGCCCGCTACTTCCAATATAGGGGTCTCTGACTACACCGCCCTGTGCCACAGGGTTC	1032
Qy	341	IleTrpThrValPheAsnGlnThrValMetLeuSerAlaYleGluIuLeuHisThrLeuSer	360
Dp	1033	ATCTGAGCTGTGTTTAACACAGCAGTGATGTGAGTGCTTAACAGAGCTCCACACCTCTCT	1092
Qy	361	AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
Dp	1093	GACACCCGTGGGGACCTGTGTACTCTCGGCTAACGCTGAATCTTCGACACGAGCGCT	1152
Qy	381	LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerSerProArgAla	400
Dp	1153	TTGAATGGGCGAGATATTGAGGCTCTTCCCTGCTGGGTGACAGCAGTCTCGGGCT	1212
Qy	401	AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe	420
Dp	1213	GCTGAGCCAGTCCACGTGAATTCCTGCGCGGTGTGTGTGAACATCCTAACCCCTGGTTTTT	1272
Qy	421	GlyLeuLeuPheAlaValHisSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440

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Db      1273 GGCCTCCTTTTGCTGTACACAGCGTCGCTTCTTGTCAGATGAGAGGACACACAGA 1332
Oy      441 ArgyIyThLyGlyGlyValSerIyArgProAlGluValAlaGluIyThrGlyAla 459
Db      1333 AGGGGAACCAAGGGGGGTGTAGCTACCGCCAGCAGAGGTACCGCAGACTGAGAGCC 1389

RESULT 8
US-09-954-456-89
; Sequence 89, Application US/09954456
; Patent No. US20020115057A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Cance
; FILE REFERENCE: 689290-76
; CURRENT APPLICATION NUMBER: US/09/954,456
; CURRENT FILING DATE: 2001-09-18
; PRIOR APPLICATION NUMBER: US/60/233,617
; PRIOR FILING DATE: 2000-09-18
; PRIOR APPLICATION NUMBER: US/60/234,052
; PRIOR FILING DATE: 2000-09-20
; PRIOR APPLICATION NUMBER: US/60/234,923
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,134
; PRIOR FILING DATE: 2000-09-25
; PRIOR APPLICATION NUMBER: US/60/235,637
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,638
; PRIOR FILING DATE: 2000-09-26
; PRIOR APPLICATION NUMBER: US/60/235,711
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,720
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,840
; PRIOR FILING DATE: 2000-09-27
; PRIOR APPLICATION NUMBER: US/60/235,863
; PRIOR FILING DATE: 2000-09-27
; NUMBER OF SEQ ID NOS: 2276
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 89
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-954-456-89

Alignment Scores:
Pred. No.:          9,97e-228          Length:          1552
Score:             2424.00             Matches:          459
Percent Similarity: 100.00%             Conservative:      0
Best Local Similarity: 100.00%             Mismatches:       0
Query Match:       100.00%             Indels:           0
DB:                9                   Gaps:            0

US-09-967-237A-2 (1-459) x US-09-954-456-89 (1-1552)

Oy      1  MetaIaProLeuCySProSeRProITrPLeuProLeuIleIleProIaIaProGly 20
Db      43  ATGGCTCCCTCGTGGCCCCAGCCCGCTGCTGCTGATCCCGGCCCTGCTCCAGGC 102
Oy      21  LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisPProGlnArgLeu 40
Db      103  CTCATCTGTGCAACTGCTGTGCTGCACGCTGCTTCTATGCTCTGCCATCCCAAGAGTTG 162
Oy      41  ProATrMetGlnGluAspSerProLeuGlyGlyIySerSerGlyGluAspAspProLeu 60
Db      163  CCCCAGATCAGAGAGGATTTCCCTTGGGAGAGAGGCTTTCTGGGAGATGACCCACTG 222
Oy      61  GlyIyGluIyAspLeuProSeRProGluIyAspSerProArgGluIyAspProProGlyGlu 80
Db      223  GGGCGAGAGAGGATCTGGCCAGTGAAGAGATTCAACCCAGAGAGGATTCACCCCGAGAG 282
Oy      81  GluAspLeuProGlyGlyGluIyAspLeuProGlyGlyGluIyAspLeuProGluValIyPro 100

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Db 283 GAGGATCTACCTGAGAGGAGATCTACCTGAGAGGAGATCTACCTGAATTAAAGCT 342
Qy 101 LysSerGluGluGlySerLeuLysLeuProThrValGluAlaProGly 120
Db 343 AATATGAAGAAGAGGGCTCCCTGAAGATCTACCTGTTAGGCTCTCTGA 402
Qy 121 AspProGluGluProGluAspAsnAlaHisArgAspLysGlyAspAspGlnSerHis 140
Db 403 GATCTCTAAGAACCCAGATATATGCCCCAGAGCAAGAAAGGAGATACCAAGACTCAT 462
Qy 141 TTPArgTYRGlyGlyAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCCCTATGAGAGGAGCCCGCTGGCCCCGGGGTGTCCCCAGCCCTGCGGGGCGCTTC 522
Qy 161 GlnSerProValAspLysArgProGluLeuAlaAlaPheCysArgProAlaLeuArgProLeu 180
Db 523 CAGTCCCGGTTGAATATCCGCCCAAGCTGCGCGCTTCGCGCGCCCTGCGCCCCCTG 582
Qy 181 GluLeuLeuGlyPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlyHis 200
Db 583 GAATCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTCGCTGGCAACATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGlyArg 220
Db 643 AGTGTCAACTGACCTGCTCTGCGGCTAGAGATGCTCTGGGTCCCGGCGGAGGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisGlnLeuHisGlnGlyAlaAlaGlyArgProGlySerGlnHisThr 240
Db 703 CGGGCTGTGCACTCATCTGCACTGGGGGGGTGACAGGTGTCGGGCTCGAGGACACT 762
Qy 241 ValGluGlyHisArgPheProAlaGluLeuHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCGTTTCCCTCCGAGATCCAGTGTTCACCTCAAGCACCCCTTTGCC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGlu 280
Db 823 AGAGTTGACGAGGCTTGGGGCGCCCGGAGGCTGCGCGTGTGGCGCTTCTGAGAG 882
Qy 281 GluGlyProGluGluAsnSerAlaTYRGluGlnLeuLeuSerArgLeuGluGluLeuAla 300
Db 883 GAGGGCCCGGAAGAAACAGTCTCATGAGAGTGTCTGCTGCGTGAAGAAATCGCT 942
Qy 301 GluGluGlySerGluThrGlnValProGlyLeuAspLysSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGGCTCAGAGACTCAGGTCCAGAGACTGAGATATCTGCACTCTGCTCTGAC 1002
Qy 321 PheSerArgTYRPhelGlnTYRGluGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAGCCCGTACTTCCAATATGAGGGGTCTGTGACTACACCGCCCTGTGCCAGGGTGT 1062
Qy 341 IleTPTThrValPheAsnGlnThrValMetLeuSerAlaLysGlnLeuHisGlnLeuSer 360
Db 1063 ATCTGAGCTGTGTTTAACAGACAGTGAAGTGAAGTGTCAACAGCTCCACACCTCTCT 1122
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgLalaThrGlnPro 380
Db 1123 GACACCCCTGTGGGAGCTGTGTACTCTGCGCTACAGCTTAACCTCCAGAGCGAGCTT 1182
Qy 381 LeuAsnGlyArgValIleGluAlaSerPheProAlaGlyValAspSerProArgAla 400
Db 1183 TTGAATGGCGAGTATGAGGCTCTTCCCTGTGAGGTGAGCAGCAGTCTCTCGGGGT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspLysLeuAlaLeuValPhe 420
Db 1243 GCTGAGCAGTCACTGAATTCCTGCTGCTGTGAGATCATCTTGAAGCCCTGTGTTT 1302
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCTCTTTTGTCTGCTACAGCGCTCGGCTCTTGTGCAATGAGAGGAGCAGCAGA 1362
Qy 441 ArgGlyThrLysGlyGlyValSerTYRArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGAGACCAAGGGGGTGTGAGCTACCGCCAGAGAGGTAGCGAGCTGGAAGCC 1419

RESULT 9
US-09-954-456-726
Sequence 726, Application US/09954456
Patent No. US20020115057A1
GENERAL INFORMATION:
APPLICANT: Young, Paul
TITLE OF INVENTION: Process for Identifying Anti-Cancer Therapeutic Agents Using Can
TITLE OF INVENTION: Sets
FILE REFERENCE: 689290-76
CURRENT APPLICATION NUMBER: US/09/954,456
CURRENT FILING DATE: 2001-09-18
PRIOR APPLICATION NUMBER: US/60/233,617
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: US/60/234,052
PRIOR FILING DATE: 2000-09-20
PRIOR APPLICATION NUMBER: US/60/234,923
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,134
PRIOR FILING DATE: 2000-09-25
PRIOR APPLICATION NUMBER: US/60/235,637
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,638
PRIOR FILING DATE: 2000-09-26
PRIOR APPLICATION NUMBER: US/60/235,711
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,720
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,840
PRIOR FILING DATE: 2000-09-27
PRIOR APPLICATION NUMBER: US/60/235,863
PRIOR FILING DATE: 2000-09-27
NUMBER OF SEQ ID NOS: 2276
SOFTWARE: Patentin version 3.0
SEQ ID NO 726
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo sapiens
US-09-954-456-726
Alignment Scores:
Pred. No.: 9,976-228 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0
US-09-967-237A-2 (1-459) x US-09-954-456-726 (1-1552)
Qy 1 MetAlaProLeuCysPProSerProTrpLeuProLeuLeuLeuProAlaProAlaProGly 20
Db 43 ATGGCTCCCGTGTGCCCCAGCCCTGCGCTCTCTGTGATCCCGGCCCTGCTCAAGGC 102
Qy 21 LeuThrValGlnLeuLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACCTGTGCAACTCTGCTGTCACTGCTCTTCTGATGCTGTCTCAATCCCAAGGTTG 162
Qy 41 ProArgMetGlnGluAspSerProLeuGlyGlyGlySerSerGlyGlyAspAspProLeu 60
Db 163 CCCCAGATGACAGAGAGATTCCCTTGGGAGGAGGCTCTTCTGGGGAAGATGACCCACTG 222
Qy 61 GlyGluGluAspLeuProSerGluGluAspSerProArgGluGluAspProProGlyGlu 80
Db 223 GCGGAGAGAGATCTGCGCCAGTGAAGAGATTCACCAGAGAGAGATCCACCCGAGAG 282
Qy 81 GluAspLeuProGlyGlyGlyLysAspLeuProGlyGluGluAspLeuProGluValLysPro 100
Db 283 GAGGATCTACTCTGAGAGAGAGATCTACTGAGAGAGAGATCTACTGAAATTAAAGCT 342
Qy 101 LysSerGluGluGlySerLeuLysLeuProThrValGluAlaProGly 120
Db 343 AATATGAAGAAGAGGGCTCCCTGAAGATCTACCTGATCTGAGGCTCTCTGA 402

QY	121	AspProGlnGluProGlnAsnAsnAlaHisArgAspArgGluGluValAspAspGlnSerHis	140
Db	403	GATCTCTCAAGAACCCCAAGATATATGCTCCACAGGGAACAAAGAGGGATATACCAAGATCAAT	462
QY	141	TPAATGTATGATGATGValAspProProTTPProArgValSerProAlaCysAlaGlyArgPhe	160
Db	463	TGGCCCTATAGAGGGGAGCCCGCCCTTGCCCGGGGTGTCCCGAGCTGTGGCGGGCGGCTTC	522
QY	161	GlnSerProValAspTLeaArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu	180
Db	523	CAGTCCCGGTGTGAATCCGCCGCCAGCTGTGCGCTTGTGCGCGGCGCTGTGCGCCCTCG	582
QY	181	GluLeuLeuGluPheGlnLeuProProLeuProGluLeuArgLeuArgAsnGlnYHis	200
Db	583	GAACCTCTGGGCTTCCAGCTCCCGCGCTTCCAGAACTGGCTGTGGCAACATATGGCCAC	642
QY	201	SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGluTyr	220
Db	643	AGTGTGCAACTGACCTGCTCTCTGGGCTAGAGATGGCTCTGGGTCCGGGGGGAGTATC	702
QY	221	ArgAlaLeuGlnLeuHisIleuHisSTRTGlyAlaAlaGlyArgProGlySerGlnHisSThr	240
Db	703	CGGGCTCTGGACACTGATGTGACATGGGGGGGTGTGACAGTGCTGTGGGCTGTGGAGCACCT	762
QY	241	ValGlnGluYHisArgPheProAlaGlnIleHisValValHisIleuSerThrAlaPheAla	260
Db	763	GTCGAAGGCCACACGTTTCCCTTCCAGATTCACAGTGTTCACCTTCAGCACCGGCTTTGCC	822
QY	261	ArgValAspGluAlaLeuGluValArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln	280
Db	823	AGAGTTGACGAGAGCCCTTGGGGGCGCCGGGAGGCGTGGCCGTGTGGCCGCTTCTTGAG	882
QY	281	GluGlyProGluGluIleuSerAlaTyrGlnGlnLeuLeuSerArgLeuGluGluIleAla	300
Db	883	GAGGGCCCGGAAAGAAACAGTGCCTATGACAGATGTGCTGTCTGTGGAAGAAATCGCT	942
QY	301	GluGluGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp	320
Db	943	GAGGAAGGCTCAGAGACTAGGATCCAGACTGGACATATCTGCACTCTGCTGCTTGAC	100
QY	321	PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal	340
Db	1003	TTCAACCCGCTACTTCCAAATATAGGGGATCTTGACTACACCGGCTGTGCCACAGGGTGTTC	106
QY	341	IleTTPThrValPheAsnGlnThrValMetLeuSerAlaIleGlnIleuHisSThrLeuSer	360
Db	1063	ATCTGGACTGTGTTTAAACAGACAGTGAAGTCAAGCAAGCTTCACACCCCTCTCT	112
QY	361	AspThrLeuTTPGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro	380
Db	1123	GACACCTCTGTGGGAGACTGTGTACTCTCGGCTTACACTGAATCTTCCGACGACGAGCCT	118
QY	381	LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla	400
Db	1183	TTGATATGGGCGAGTATTAGGCGCTTCTTCCCTGTGGAGTGAGACAGCAGTCTCTGGGGCT	124
QY	401	AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspTLeuAlaLeuValPhe	420
Db	1243	GCTGAGCCAGCTCAGACTGAATTCCTGCGCTGTGTGGAGCAATCTTACCCCTGATTTT	130
QY	421	GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg	440
Db	1303	GGCTTCCTTTTGGCTGTCCACGAGCGTGGCTTCTTGTGCAGATGAGAGGACGACACAA	136
QY	441	ArgGlyThrLysGlyGlyValSerTyrArgProAlaGluValAlaGluThrGlyAla	459
Db	1363	AGGGGAACCAAGGGGGTGTGAGTACCGCCAGCAGAGGTATGCCAGACTGGAGCC	1419
RESULT 10			
US-09-960-706-1080			
; Sequence 1080, Application US/09960706			
; Publication No. US20030134280A1			

```

; GENERAL INFORMATION:
; APPLICANT: Mungler, William E.
; TITLE OF INVENTION: Identifying Drugs for and Diagnosis of Benign Prostatic Hyperplasia
; FILE OF INVENTION: Gene Expression Profiles
; FILE REFERENCE: 44921-5029-01US
; CURRENT APPLICATION NUMBER: US/09/960,706
; CURRENT FILING DATE: 2001-09-24
; PRIOR APPLICATION NUMBER: 60/223,323
; PRIOR FILING DATE: 2000-08-07
; PRIOR APPLICATION NUMBER: 09/873,319
; PRIOR FILING DATE: 2001-06-05
; NUMBER OF SEQ ID NOS: 1124
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1080
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: Genbank Accession No. US20030134280A1 X66839
US-09-960-706-1080

Alignment Scores:
Score, No.:          9,97e-228          Length:          1552
Percent Similarity: 2424.00             Matches:          459
Best Local Similarity: 100.00%           Conservative:      0
Query Match:         100.00%           Mismatches:      0
DB:                  10                Indels:          0
                       Gaps:           0

US-09-967-237A-2 (1-459) x US-09-960-706-1080 (1-1552)

QY      1      MetaIaProleuCysProSerProTrieuProleuIleuIleProIaIaProIaProGly 20
DB      43      ATGGCTCCCTGTGCCCCAGCCCTTGCTCCCTCTGTGATCCCGGCCCTGCTCCAGGC 102
QY      21      LeuThrValGlnLeuLeuLeuSerLeuLeuLeuLeuMetProValHisProGlnArgLeu 40
DB      103     CTCACCTGTGCAACTGCTGCTGTCACCTGCTTCTATGCTTCATGCCCTGCCACAGAGTTG 162
QY      41      ProAGMetGlnGluAspSerProLeuGlyGlySerSerGlyGluAspAspProLeu 60
DB      163     CCCCCGATCAGAGAGATTCCCCCTTGGAGAGAGGCTCTTCTGCGGAAGATGACCCACTG 222
QY      61      GlyGlnGluAspLeuProSerGlnGluAspSerProArgGlnGluAspProProGlyGlu 80
DB      223     GGCGAGAGAGATCTGCGCCAGTGAAGAGATTCCACCAGAGAGAGATCCACCGGAGAG 282
QY      81      GluAspLeuProGlyGlyGlnGluAspLeuProGlyGlyGlnGluAspLeuProGlyValValysPro 100
DB      283     GAGGATCTAACCAGAGAGAGGATCTCACTGAGAGAGAGATCTACTGTAAGTTAACTT 342
QY      101     LysSerGlnGlnGlnGlySerLeuLysLeuGluAspLeuProThrValGlnAlaProGly 120
DB      343     AATATCAAGAAAGAGGCTCCCTGAGATTAGAGGATCTTACTTCTGTTGAGCTCTCGGA 402
QY      121     AspProGlnGluProGlnAsnAsnAlaHisArgAspLysGlnGlyAspAspGlnSerHis 140
DB      403     GATCTCTCAAGAACCCACAGATATATGCCACAGGGAACAAGAGGGATGACAGAGTCAT 462
QY      141     TrpArgTyrGlyGlyAspProProTyrProAlaValSerProAlaCysValArgValPhe 160
DB      463     TGGCCCTATGAGAGGCAACCGCCCTGCGCCCGGATCTCCACACCTGCGCGGCGGCTTC 522
QY      161     GlnSerProValAspLysArgProGlnLeuAlaAlaPheCysAspProAlaLeuArgProLeu 180
DB      523     CAGTCCCCCGGTGATATCCGCCCCACAGCTCGCGCTTCTGCCCCGGCCCTGCGCCCCCTG 582
QY      181     GluLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnGlnHis 200
DB      583     GAACCTCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGGGCAACATGGCCAC 642
QY      201     SerValGlnLeuThrLeuProProGlyLeuGluMetAlaLeuGlyProGlyArgGluTyr 220

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643 AGTGTCAACTGACCCCTGCTCTGGGGCTAGAGATGCTGTGGTCCCGGGCGGAGTAC 702
Qy ArgAlaLeuGlnLeuHisLeuHisIleThrGlyAlaAlaGlyArgProGlySerGlnHisIleThr 240
Db CGGGCTGTGACAGCTGATCTGTGACTGGGGGCTGTGAGGGTGTCCGGCTCGGAGCACT 762
Qy ValGlnGlyHisArgPheProAlaGlnIleHisValHisLeuSerThrAlaPheAla 260
Db GTGGAGGCGCACCGTTTCCCTGCCGAGATCCAGTGGTTCACTGACCTACGACCGCCCTTGGC 822
Qy ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln 280
Db AGAGTTGACGAGAGCTTGGGGGCGCCGGGAGGCGTGGCGTGTGGCCCTTTCTGGAG 882
Qy GlnGlyArgProGlnGlnAsnSerAlaTyrGlnGlnLeuLeuSerArgLeuGlnGlnIleAla 300
Db GAGGCGCCGGAAGAAACAGATGCTATAGACGTTGTCTGCTCCGCTTGGAAATAATCCCT 942
Qy GlnGlnGlySerGlnThrGlnValArgProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db GAGGAGGCTCAGAGACTCAGGTCCAGGACTGGACATATCTGCACTCTGCTCCCTGAC 1002
Qy PheSerArgTyrPheGlnTyrGlnGlySerLeuThrProProCysAlaGlnGlyVal 340
Db TTCAAGCCCTACTTCCATATAGAGGGGTCTGACTACACCGCCCTGTGCCAGGGGTGC 1062
Qy IleThrThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisIleThrLeuSer 360
Db ATCTGACTGTGTATACCAAGACAGTGAATGCTGAATGCTGAAGCACTCCACACCTCTCT 1122
Qy AspThrLeuTyrGlyArgProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db GACACCCCTGTGGGAGCTGTGTGACTCTGGCTACAGCTGAACTTCCGAGCGACGAGCT 1182
Qy LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProAla 400
Db TTGAATGGCGAGATGATGAGGCTCTTCCCTGCTGAGTGAAGACAGAGTCCCTGGGCT 1242
Qy AlaGlnProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db GCTAGCCAGTCCAGCTGAATTCCTGCTGTGTGTGACATCTGAGCCCTGTTTTTT 1302
Qy GlnLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db GGCTCTCTTTTCTGCTGACCAAGCTCCGCTTCTTGTGCAGATGAGAAAGCAGACAGA 1362
Qy ArgGlyThrIlyGlyGlyValSerTyrArgProAlaGlnValAlaGlnThrGlyAla 459
Db AGGGGAACCAAGGGGGTGTGAGCTACCGCCAGAGAGTACCGGAGACTGGAGCC 1419

RESULT 11
US-09-873-367C-516
; Sequence 516, Application US/09873367C
; Publication No. US20030165839A1
; GENERAL INFORMATION:
; APPLICANT: Young, Paul
; APPLICANT: Soppet, Daniel
; APPLICANT: Endreese, Gregory
; APPLICANT: Augustus, Weena
; APPLICANT: Ebner, Reinhard
; APPLICANT: Carter, Kenneth
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using
; TITLE OF INVENTION: Signature Gene Sets
; FILE REFERENCE: 689290-64
; CURRENT APPLICATION NUMBER: US/09/873, 367C
; CURRENT FILING DATE: 2003-04-29
; PRIOR APPLICATION NUMBER: U.S. 60/236, 891
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/236, 842
; PRIOR FILING DATE: 2000-09-29
; PRIOR APPLICATION NUMBER: U.S. 60/244, 867
; PRIOR FILING DATE: 2000-11-01
; PRIOR APPLICATION NUMBER: U.S. 60/245, 084

PRIOR FILING DATE: 2000-11-01
; NUMBER OF SEQ ID NOS: 1067
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 516
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-873-367C-516

Alignment Scores:
Pred. No.: 9,976-228 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 10 Gaps: 0

US-09-967-237A-2 (1-459) x US-09-873-367C-516 (1-1552)

Qy 1 MetaLAPProLeuCyProSerProThrLeuProLeuLeuIleProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGTGCCCCAGCCCTGTGCTCTCTGTGTGATCCGGCCCTGTGCTCAGGC 102
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACGTGCAACTGCTCTGTCTGTCACTGTCTGTGTGATGCTTGTGATGCTTGTGATGCTTGTG 162
Qy 41 ProArgMetGlnLysAspSerProLeuGlyGlySerGlyGlyLysAspProLeu 60
Db 163 CCCCAGATGCAAGAGGATTTCCCTTGGGAGAGGCTTCTGTGGGAGATGACCCACTG 222
Qy 61 GlnGlnGlnLysAspProSerGlnLysAspSerProArgGlnGlnLysAspProGly 80
Db 223 GCGAGAGAGATCTGCCCCAGTGAAGAGATTCACCCAGAGAGAGATTCACCCGAGAG 282
Qy 81 GlnAspLeuProGlyGlnGlnLysAspProGlyGlnGlnLysAspLeuProGlnValLysPro 100
Db 283 GAGATCTACTGAGAGAGAGATCTACTGAGAGAGATCTACTGAGATTAAGCT 342
Qy 101 LysSerGlnGlnGlnGlySerLeuLysLeuGlnLysAspProThrValGlnAlaProGly 120
Db 343 AAATCAGAAAGAGGGCTCTCCTGAAGTAAAGATTAAGTACTGTTGAGGCTCTTGA 402
Qy 121 AspProGlnGlnProGlnAsnAsnAlaHisArgAspIlyGlnGlyAspAspGlnSerHis 140
Db 403 GATCTCAAGAACCCCAAGATTAATGCCACAGGACAAAGAGGAGATCAAGATAT 462
Qy 141 TyrArgTyrGlyGlyAspProProThrProAlaSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGGCTATGAGAGGCGACCGCCCTGGCCCGGGGTGTCCAGGCTGGCGGGCGGCTTC 522
Qy 161 GlnSerProValAspIleArgProGlnLeuAlaAlaPheCysProAlaLeuAspProLeu 180
Db 523 CAGTCCCGGGTGGATATCCGCCCCAGCTGCGCCCTTGTGCCCCGGCCCTGCCCCCTG 582
Qy 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnAsnGlnHis 200
Db 583 GAATCTCTGGGCTTCCAGCTCCCGCTCCCAABAATCGGCTGCGGACAAATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyLeuGlnMetAlaLeuGlyProGlyArgGlnTyr 220
Db 643 AGTGTCAACTGACCCCTGCTCCCTGGGCTAGAGATGCTGTGGTCCCGGGCGGAGTAC 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisIleThrGlyAlaAlaGlyArgProGlySerGlnHisIleThr 240
Db 703 CGGGCTGTGACAGCTGATCTGTGACTGGGGGCTGTGAGGGTGTCCGGCTCGGAGCACT 762
Qy 241 ValGlnGlyHisArgPheProAlaGlnIleHisValHisLeuSerThrAlaPheAla 260
Db 763 GTGGAGGCGCACCGTTTCCCTGCCGAGATCCAGTGGTTCACTTCAAGACCGCCCTTGGC 822
Qy 261 ArgValAspGlnAlaLeuGlyArgProGlyGlyLeuAlaValLeuAlaAlaPheLeuGln 280

Db 823 AGAGTTGACGAGGCGCTTGGGCGCCGCGAGGCGCTGGCGCTGTGTGCGCCCTTTCTTGAG 882
Qy 281 GUGUlyProgluGluAaNSerAlaTyrgluGluInleuNSerArgeuGluGluAla 300
Db 883 GAGGGCCCGGAGAAACAGTGTCTATGAGCAGTTGCTGTCTGCTTGAGAAATGCT 942
Qy 301 GUGUlySerGluThrgluInValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGCTCAGAGACTCAGGTCCAGAGACTGACATATCTGCATCTCGCCCTTGAC 1002
Qy 321 PheSerArgTyrrPheGlnTyrgluGlySerleuThrrProProCysAlaGlnGlyVal 340
Db 1003 TTCAGCGCTACTTCATATGAGGGGTCTCTGACTACCGCCCTGTGCGCAGGTC 1062
Qy 341 lIetrPthrValPheAaGlnThrValMetLeuSerAlaIysGlnLeuHlsthLeuSer 360
Db 1063 ATCTGCACTGTGTTTAAACAGACAGTATGCTGAGTCTAAGACGCTCCACACCTCTCT 1122
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgleuGlnLeuAaPheArgAlaThrGlnPro 380
Db 1123 GACACCTGTGGGAGCTGGTGACTCTGGCTACAGCTGAACCTCCGAGCGACGACCT 1182
Qy 381 LeuAaNSerArgValIleGluAlaSerPheProAlaGlyValAaSerSerProArgAla 400
Db 1183 TTGAATGGCGAGATGAGAGCTCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1242
Qy 401 AlagluProValGlnLeuAaNSerCysLeuAlaIaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCGACTCCAGCTGGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
Qy 421 GlyLeuLeuPheAlaValIleSerValAlaPheLeuValGlnMetArgArgGlnHleArg 440
Db 1303 GGCTCTCTTTTGTCTGCTACAGCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1462
Qy 441 ArgGlyThrIysGlyValSerTyrrArgProAlaGluValAlaGluThrglyAla 459
Db 1363 AGGGAAACAAAGGGGTGTGAGCTACCGCCACAGAGGTAGCCGAGACTGAGGCC 1419

RESULT 12
US-09-968-007A-213
; Sequence 213, Application US/09968007A
; Publication No. US20040115625A1
; GENERAL INFORMATION:
; APPLICANT: Ebner, Reinhard
; TITLE OF INVENTION: Cancer Gene Determination and Therapeutic Screening Using Signa
; TITLE OF INVENTION: Gene Sets
; FILE REFERENCE: 689290-71
; CURRENT APPLICATION NUMBER: US/09/968,007A
; CURRENT FILING DATE: 2001-10-02
; PRIOR APPLICATION NUMBER: US/60/237,172
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,173
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,278
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,294
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,295
; PRIOR FILING DATE: 2000-10-02
; PRIOR APPLICATION NUMBER: US/60/237,316
; PRIOR FILING DATE: 2000-10-02
; NUMBER OF SEQ ID NOS: 1001
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 213
; LENGTH: 1552
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-968-007A-213

Alignment Scores:
Pred. No.: 9,97e-228 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0

Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
DB: 11 Gaps: 0
US-09-967-237a-2 (1-459) x US-09-968-007A-213 (1-1552)

Qy 1 MetAlaProLeuCysProSerProTrpLeuProLeuLeuIleProAlaProAlaProGly 20
Db 43 ATGGCTCCCTGTGGCCCAAGCCCTCGGCTCCTCTGTGATCCCGGCCCTGCTCAGGC 102
Qy 21 LeuThrValGlnLeuLeuLeuSerleuLeuLeuMetProValHlsProGlnArgLeu 40
Db 103 CTGACTGTGCACTGTGCTGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 162
Qy 41 ProArgMetGlnIleuAspSerProLeuGlyGlyIleSerSerGlyIleuAspAppProLeu 60
Db 163 CCCCGATGAGAGAGATTCCTCCCTTGGAGAGAGCTCTTCTGGGAAGATGACCACTG 222
Qy 61 GlyGluGluAspLeuProSerGluIleuAspSerProArgGluIleuAspProProGlyIle 80
Db 223 GCGGAGGAGATCTGCCAGTGAAGAGATTCAACCAGAGAGAGATCCACCCGAGAG 282
Qy 81 GluAspLeuProGlyIleGluIleuAspLeuProGlyIleGluIleuAspLeuProGlyIlePro 100
Db 283 GAGGATCTTACTGAGAGAGAGATCTTACTGAGAGAGATCTTACTGAGAGATCTTACTGAG 342
Qy 101 lYsSerGluGluGluGlySerLeuIleuGluIleuAspLeuProThrValGluAlaProGly 120
Db 343 AAATCAGAAAGAGAGGCTCCCTGAAATTAGAGATCTTACTGAGATCTTACTGAGATCTT 402
Qy 121 AspProGlnIleuProGlnAaNSerAlaHlsArgAspIleGluIleuAspIleuSerHls 140
Db 403 GATCTCAAGAAACCCAGATATATGCCACAGGGAAGAGAGATGCCAGATGCTCAT 462
Qy 141 TrpArgTyrglyIleuAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCGCTAG 522
Qy 161 GlnSerProValAspIleArgProGlnIleuAlaIaPheCysProAlaLeuArgProLeu 180
Db 523 CATCTCCCGGTGATATCCGCCCAAGCTGCGGCTTGTGCGCCGCGCCCTGCGCCCTG 582
Qy 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAaNSerGlyHls 200
Db 583 GAACCTCTGGGCTTCAGAGCTCCCGCGCTCCAGAACTGGCGCTGCGCAACATGCGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyIleuGlnMetAlaLeuGlyProGlyArgGlyIle 220
Db 643 AGTGTCACTGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 702
Qy 221 ArgAlaLeuGlnLeuHlsLeuHlsIleuIleuAlaIaGlyArgProGlySerGluHlsThr 240
Db 703 CGGCTCTGAGCTGATCTGCACTGGGGGGGTGCAAGTCTGCTGCGGCTCGAGCACACT 762
Qy 241 ValGluGlyHlsArgPheProAlaGluIleHlsValIleHlsLeuSerThrAlaPheAla 260
Db 763 GTGAAGGCCACCGTTTCTGCTGCGAGATCCAGTGTTCACCTCGACACCGCTTTGCC 822
Qy 261 ArgValAspGluAlaLeuGlyArgProGlyIleuAlaValLeuAlaIaPheLeuGlu 280
Db 823 AGAGTTGACGAGGCTTGGGGCCCGGGAGGCTGCGGTGTGGCGGCTTTCTTGAG 882
Qy 281 GUGUlyProgluGluAaNSerAlaTyrgluGluInleuNSerArgeuGluGluAla 300
Db 883 GAGGGCCCGGAGAAACAGTGTCTATGAGCAGTTGCTGTCTGCTTGAGAAATGCT 942
Qy 301 GUGUlySerGluThrgluInValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGCTCAGAGACTCAGGTCCAGAGACTGACATATCTGCATCTCGCCCTTGAC 1002
Qy 321 PheSerArgTyrrPheGlnTyrgluGlySerleuThrrProProCysAlaGlnGlyVal 340
Db 1003 TTCAGCGCTACTTCATATGAGGGGTCTCTGACTACCGCCCTGTGCGCAGGTC 1062

Qy 341 ILeTrrThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisThrLeuSer 360
Db 1063 ATCTGGACTGTGTTTAACCAAGACAGTGAATGCTGAGGTGCTAACACCTCCACCTCTCT 1122
Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCCCTGTGGGAGACTGTGACTCTCGGCTACAGCTGAACCTCCGAGCGACGAGCT 1182
Qy 381 LeuAsnGlyArgValIleGlnAlaSerPheProAlaGlyValAspSerSerProArgAla 400
Db 1183 TTGAATGGCGCAGTGAATGAGGCTCTCTCCCTGCTGAGTGAACAGACAGTCTCTGGGCT 1242
Qy 401 AlaGluProValGlnLeuAsnSerCysLeuAlaAlaGlyAspIleLeuAlaLeuValPhe 420
Db 1243 GCTGAGCCAGTCCACCTGAATTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1302
Qy 421 GlyLeuLeuPheAlaValThrSerValAlaPheLeuValGlnMetArgArgGlnHisArg 440
Db 1303 GGCCTCTTTTGTCTGTCAACGCGCTCGGCTCTTGTGACAGATGAGAAAGCAGCAGCA 1362
Qy 441 ArgGlyThrIleGlyValSerIleArgProAlaGluValAlaGluThrGlyAla 459
Db 1363 AGGGGAAACCAAGGGGTGTGAGTACCGCCAGCAGAGTAGCCGAGACTGGAGCC 1419

RESULT 13

US-10-301-822-11
Sequence 11, Application US/10301822
Publication No. US20030148410A1
GENERAL INFORMATION:
APPLICANT: Millennium Pharmaceuticals, Inc.
APPLICANT: Berger, Allison
APPLICANT: Guillemette, Tracy L.
APPLICANT: Kamatkar, Shubhangi
APPLICANT: Schlegel, Robert
APPLICANT: Monahan, John E.
APPLICANT: Thibodeau, Stephen N.
APPLICANT: Burgart, Lawrence J.
TITLE OF INVENTION: NOVEL GENES, COMPOSITIONS, KITS, AND
TITLE OF INVENTION: METHODS FOR IDENTIFICATION, ASSESSMENT, PREVENTION, AND
TITLE OF INVENTION: THERAPY OF COLON CANCER
FILE REFERENCE: MP001-029P2RNM
CURRENT APPLICATION NUMBER: US/10/301,822
CURRENT FILING DATE: 2002-11-21
PRIOR APPLICATION NUMBER: US 60/339,971
PRIOR FILING DATE: 2001-12-10
PRIOR APPLICATION NUMBER: US 60/361,978
PRIOR FILING DATE: 2002-03-05
PRIOR APPLICATION NUMBER: US 60/381,988
PRIOR FILING DATE: 2002-05-20
NUMBER OF SEQ ID NOS: 228
SOFTWARE: FastSeq For Windows Version 4.0
SEQ ID NO 11
LENGTH: 1552
TYPE: DNA
ORGANISM: Homo Sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (43) ... (1422)
US-10-301-822-11

Alignment Scores:

Pred. No.: 9,97e-228 Length: 1552
Score: 2424.00 Matches: 459
Percent Similarity: 100.00% Conservative: 0
Best Local Similarity: 100.00% Mismatches: 0
Query Match: 100.00% Indels: 0
Gaps: 0

US-09-967-237a-2 (1-459) x US-10-301-822-11 (1-1552)

Qy 3 MetalProLeuCyProSerProTrpLeuProLeuLeuProAlaProAlaProGly 20
|||||

Db 43 ATGGCTCCCTGTGCCCCAGCCCTGCTCTCTGTTGATCCCGGCCCTGCTCCAGGC 102
Qy 21 LeuThrValGlnLeuLeuSerLeuLeuMetProValHisProGlnArgLeu 40
Db 103 CTCACTGGCAACCTGCTGTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 162
Qy 41 ProArgMetGlnGlyAspSerProLeuGlyGlySerSerGlyGlyAspAspProLeu 60
Db 163 CCCCGATGACAGAGATTTCCCTTGGGAGAGAGCTTTCTGGGAGAGATGACCATCTG 222
Qy 61 GlyGlnAspLeuProSerGlnGlyAspSerProArgGlnGlyAspProGlyGly 80
Db 223 GCGCAGAGAGATCTGCCAGTGAAGAGATTCACCAAGAGAGAGATCCACCCGAGAG 282
Qy 81 GlnAspLeuProGlyGlyGlnAspLeuProGlyGlyGlnAspLeuProGlyValLysPro 100
Db 283 GAGATCTTACCTGAGAGAGAGATTTACTGAGAGAGAGATCTTACCTGAAATTAGCT 342
Qy 101 LysSerGlnGlnGlnGlySerLeuLysLeuGlyAspLeuProThrValGlnAlaProGly 120
Db 343 AATCAAGAAAGAGAGCTCCCTGAAATTAAGATCTTACTGTTGAGGCTCTGGA 402
Qy 121 AspProGlnGlnProGlnAsnAsnAlaHisArgAspLysGlyGlyAspAspGlnSerHis 140
Db 403 GATCCTCAAGAAACCCAGAAATTAATGCCACAGAGCAAAAGAGGAGTACACAGAGTCAT 462
Qy 141 TTPArgTyrGlyIleAspProProTrpProArgValSerProAlaCysAlaGlyArgPhe 160
Db 463 TGGCGCTATGAGAGGAGACCCGCTGCGCGCGCGCGCGCGCGCGCGCGCGCTTC 522
Qy 161 GlnSerProValAlaPheArgProGlnLeuAlaAlaPheCysProAlaLeuArgProLeu 180
Db 523 CAGTCCCGGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 582
Qy 181 GlnLeuLeuGlyPheGlnLeuProProLeuProGlnLeuArgLeuArgAsnArgHis 200
Db 583 GAATCCTGGGCTTCCAGCTCCCGCGCTCCAGAACTGGCGCTGCGCAACAATGGCCAC 642
Qy 201 SerValGlnLeuThrLeuProProGlyGlnGlnMetAlaLeuGlyProGlyArgGlnLys 220
Db 643 AGTGTCAACAGACCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 702
Qy 221 ArgAlaLeuGlnLeuHisLeuHisGlyProGlyAlaAlaGlyArgProGlyLysGlnHisThr 240
Db 703 CGGCTCTGACGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 762
Qy 241 ValGlnGlyHisArgPheProAlaGlnIleHisValAlaHisLeuSerThrAlaPheAla 260
Db 763 GTGGAAGGCCACCGTTTCCCTGCCAGATCCACGAGTTCACTCAGCAGCAGCCCTTTC 822
Qy 261 ArgValAspGlnAlaLeuGlyValArgProGlyGlyLeuAlaValIleLeuAlaPheLeuGln 280
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Qy 301 GlnGlnGlySerGlnThrGlnValProGlyLeuAspIleSerAlaLeuLeuProSerAsp 320
Db 943 GAGGAAGGCTCAGAGACTCAGGCTCCAGAGCTGACATATCTGCACTCTCCCTCTGAC 1002
Qy 321 PheSerArgTyrPheGlnTyrGlnGlySerLeuThrThrProProCysAlaGlnGlyVal 340
Db 1003 TTCAAGCGCTACTTCAATATAGAGGGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1062
Qy 341 ILeTrrThrValPheAsnGlnThrValMetLeuSerAlaValGlnLeuHisThrLeuSer 360
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Qy 361 AspThrLeuTrpGlyProGlyAspSerArgLeuGlnLeuAsnPheArgAlaThrGlnPro 380
Db 1123 GACACCCCTGTGGGAGACTGTGACTCTCGGCTACAGCTGAACCTCCGAGCGAGCAGCT 1182


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TITLE OF INVENTION: Diagnosis and Prognosis of Breast Cancer Patients
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